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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:21:45 ; Search time 35.4545 seconds
(without alignments)
30.067 Million cell updates/sec

Title: US-09-543-188a-1
Perfect score: 55
Sequence: 1 GWCOPHCG 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues
Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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22: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	8	23 AABU1824	Prion protein, PrP
2	55	100.0	11	23 AABU1629	Prion mimetic pept
3	55	100.0	14	22 AABU4521	Octa-peptide motif
4	55	100.0	16	23 AABU1825	Prion protein, PrP
5	55	100.0	16	23 AABU1856	Prion protein, PrP
6	55	100.0	18	14 AAB38026	Bovine prion prote
7	55	100.0	18	14 AAB38029	Ovine prion protei
8	55	100.0	18	14 AAB38032	Human prion protei
9	55	100.0	26	14 AAB38035	Prion protein regi
10	55	100.0	42	20 AAY07999	Bovine prion prote

11	55	100.0	178	19 AAB70280	Peptide sequences
12	55	100.0	208	21 AAB07316	Mouse prion protei
13	55	100.0	208	21 AAB07318	Mouse prion protei
14	55	100.0	208	21 AAB07327	Mouse prion protei
15	55	100.0	208	21 AAB07329	Human prion protei
16	55	100.0	208	22 AAB82110	Hamster PrP peptid
17	55	100.0	208	23 AAB15601	Hamster PrP protei
18	55	100.0	211	22 AAB30801	Amino acid sequenc
19	55	100.0	212	22 AAB30802	Amino acid sequenc
20	55	100.0	217	21 AAB07317	Cattle prion prote
21	55	100.0	217	21 AAB07328	Cattle prion prote
22	55	100.0	219	19 AAB70261	Bovine prion prote
23	55	100.0	219	20 AAB93571	Bovine prion prote
24	55	100.0	245	22 AAB72342	Monkey prion prote
25	55	100.0	245	22 AAB72352	Cercopithecus prion p
26	55	100.0	250	22 AAB72369	Rabbit prion prote
27	55	100.0	253	17 AAB86715	Human prion protei
28	55	100.0	253	19 AAB65660	Human prion protei
29	55	100.0	253	20 AAY07994	Human prion protei
30	55	100.0	253	20 AAB85901	Human prion protei
31	55	100.0	253	21 AAB15035	Human prion protei
32	55	100.0	253	21 AAB06272	Human PrP prion pr
33	55	100.0	253	21 AAY81485	Human prion protei
34	55	100.0	253	22 AAB65853	Human prion protei
35	55	100.0	253	22 AAB82112	Human PrP. Homo s
36	55	100.0	253	22 AAB72338	Human prion protei
37	55	100.0	253	22 AAB72339	Chimpanzee prion p
38	55	100.0	253	22 AAB72340	Orangutan prion pr
39	55	100.0	253	22 AAB72341	Corilla prion prot
40	55	100.0	253	22 AAB72344	Rhesus monkey prio
41	55	100.0	253	22 AAB72345	Gibbon prion prote
42	55	100.0	253	22 AAB72346	Prion protein cell
43	55	100.0	253	22 AAB72347	Prion protein cell
44	55	100.0	253	22 AAB72348	Prion protein cell
45	55	100.0	253	22 AAB72349	Prion protein cell

ALIGNMENTS

RESULT 1	AAU11824	standard; peptide; 8 AA.
ID	AAU11824	
AC	AAU11824	
DF	26-MAR-2002	(first entry)
DE	Prion protein, PrP, octapeptide motif.	
XX	Prion protein, PrP, ligand; octapeptide motif; scrapie;	
KW	Prion-associated disease; Creutzfeldt-Jakob disease;	
KW	Gerstmann-Strausler-Scheinker disease; fatal familial insomnia;	
KW	feline spongiform encephalopathy; bovine spongiform encephalopathy;	
KW	transmissible mink encephalopathy; exotic ungulate encephalopathy;	
KW	chronic wasting disease.	
OS	Mammalia.	
XX		
PN	WO200177687-A2.	
XX		
PD	18-OCT-2001.	
XX		
PF	05-APR-2001; 2001WO-US11150.	
XX		
PR	05-APR-2000; 2000US-0543188.	
XX		
PA	(VITE-) VI TECHNOLOGIES INC.	
XX		
PI	Hammond DJ, Wiltshire VR, Carbonell R, Shen H;	
XX		
DR	WPI: 2002-061944/08.	
XX		

PT New ligands for prion proteins, useful for detection or removal or
PT prions and for treating prion-associated diseases, recognize a specific
PT octapeptide motif -

Claim 1; Page 33; 47pp; English.

CC The invention relates to a ligand of less than 6 kD that binds to a
CC polypeptide containing the sequence GLYTRIGLYNPROHISGLYGLY (A) or an
CC analogue that is the retro-inverso isomer of (A). The sequence A is
CC an octapeptide motif from the prion protein (PrP). The ligands are
CC identified by binding assays with the peptide (A) or peptides containing
CC (A). The ligands are used for detecting prion proteins (or prions) in
CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jakob diseases (in
CC iatrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strausler-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is the PrP octapeptide A.

Sequence 8 AA:

Query Match 100.0%; Score 55; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
Db 1 GWGPHHG 8

RESULT 2

ABB81629
ID ABB81629 standard; peptide: 11 AA.

XX ABB81629;

DT 25-SEP-2002 (first entry)

DE Prion mimetic peptide SEQ ID NO:1.

XX Prion mimetic peptide; degradation; TSE; infection;
KW transmissible spongiform encephalopathy; prion protein; sterilisation;
KW immunisation; Creutzfeldt-Jacob disease; kuru; fatal familial insomnia;
KW Gerstmann-Strausler-Scheinker syndrome; chronic wasting disease;
KW bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW scrapie; transmissible mink encephalopathy.

Synthetic.

PN WO200253723-A2.

PD 11-JUL-2002.

PF 08-JAN-2002; 2002WO-GB00052.

PR 08-JAN-2001; 2001GB-0000420.

PR 26-FEB-2001; 2001GB-0004696.

PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.

PI Raven NDH;

WP1; 2002-557743/59.

PT Inactivating transmissible spongiform encephalopathy (TSE) agent such
PT as Creutzfeldt-Jacob disease, scrapie, kuru or
PT Gerstmann-Strausler-Scheinker syndrome involves exposing agent to
PT thermostable proteolytic enzyme -
XX Example; Page 19; 41pp; English.

CC The present invention describes a method (M1) for inactivating a
CC transmissible spongiform encephalopathy (TSE) agent comprising exposing
CC the TSE agent to a thermostable proteolytic enzyme. Also described:
CC (1) a composition (I) for inactivating a TSE agent, comprising a
CC thermostable proteolytic enzyme; (2) an antibody (II) specific for a
CC prion dimer which does not bind to a prion monomer; and (3) a purified
CC prion dimer. (M1) is useful for inactivating a TSE agent such as a prion.

CC A TSE agent is Creutzfeldt-Jacob disease or its variant, kuru, fatal
CC familial insomnia, Gerstmann-Strausler-Scheinker syndrome, bovine
CC spongiform encephalopathy, scrapie, feline spongiform encephalopathy,
CC chronic wasting disease or transmissible mink encephalopathy. (I) is
CC useful for sterilising material contaminated with the TSE agent. A prion
CC dimer is useful for examining a sample infected with or suspected to be
CC infected by a prion protein, and for detecting prion infectivity, by
CC detecting a prion dimer in the sample. A prion dimer is useful for
CC producing (II), by immunising an animal with a prion dimer, obtaining its
CC extract which contains (II), and isolating (II) from the extract. The
CC method comprises obtaining an antibody preparation containing antibodies
CC which bind a prion dimer, and removing (II) from the preparation. (M1)
CC and (I) are useful for inactivating TSE agents in potentially
CC contaminated clinical waste and culled animal material. (M1) is useful
CC for sterilising larger surface areas of apparatus, operating tables or
CC even walls of rooms. The present sequence represents a prion mimetic
CC peptide which is used in an example from the present invention in the
CC preparation of antibodies including dimer preferential antibodies.

Sequence 11 AA:

Query Match 100.0%; Score 55; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
Db 3 GWGPHHG 10

RESULT 3

ABB84521
ID ABB84521 standard; peptide: 14 AA.

XX ABB84521;

DT 05-SEP-2001 (first entry)

DE Octa-peptide motif repeated in human prion protein.

XX Prion protein; subacute transmissible spongiform encephalopathy; ESST;
KW Creutzfeld-Jakob disease; bovine spongiform encephalopathy; scrapie.

XX Homo sapiens.

PN WO200135104-A1.

PD 17-MAY-2001.

PF 13-NOV-2000; 2000WO-FR03159.

PR 12-NOV-1999; 99FR-0014242.

PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PI Deslys J, Comoy E, Grassi J;

WP1; 2001-408079/43.

PT Diagnosis of prion diseases, by treatment with proteinase K and
PT detecting retention of octapeptide repeat motifs, including
PT differentiation between prion strains -
XX Example 1; Page 13; 51pp; French.

XX The present sequence represents an octa-peptide repeat motif of a

CC prion protein. The specification describes a method for the diagnosis
CC of subacute transmissible spongiform encephalopathy (ESST) caused by a
CC strain of unconventional transmissible agent. The method comprises
CC detecting abnormal prion protein in a biological sample. The sample is
CC treated with at least one proteinase K while retaining at least some of
CC the octapeptide repeats in the prion protein, then treatment with a
CC 119 and for octapeptide repeats and detecting any formation of a complex.
CC The method is used to diagnose ESST, particularly (new variant)
CC Creutzfeldt-Jakob diseases, bovine spongiform encephalopathy and
CC scrapie.

XX Sequence 14 AA:

Query Match 100.0%; Score 55; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGG 8
| | | | | | | |
2 GWGPHGG 9

RESULT 4
AAU11825

ID AAU11825 standard; peptide; 16 AA.

XX AC AAU11825;

DT 26-MAR-2002 (first entry)

XX DE Prion protein, PrP, octapeptide motif containing peptide.

KW Prion protein; PrP; ligand: octapeptide motif; scrapie;
KW prion-associated disease; Creutzfeldt-Jakob disease;
KW Gerstmann-Strausser-Scheinker disease; fatal familial insomnia;
KW feline spongiform encephalopathy; bovine spongiform encephalopathy;
KW transmissible mink encephalopathy; exotic ungulate encephalopathy;
KW chronic wasting disease.

XX OS Mammalia.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "Gly is acetylated"

FT Modified-site 16 /note= "Gly is amidated"

XX FT

XX WO200177687-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US11150.

XX PR 05-APR-2000; 2000US-0543188.

XX PA (VITE-) VI TECHNOLOGIES INC.

XX PI Hammond DJ, Wiltshire VR, Carbonell R, Shen H;

XX DR WPI; 2002-061944/08.

XX PT New ligands for prion proteins, useful for detection or removal or

XX PR prions and for treating prion-associated diseases, recognize a specific

XX PS octapeptide motif -

XX CC Claim 1; Page 33; 47pp; English.

XX The invention relates to a ligand of less than 6 kD that binds to a
XX polypeptide containing the sequence GlyTyrGlyInPrOHISGlyGly (A) or an
XX analogue that is the retro-inverse isomer of (A). The sequence A is
XX an octapeptide motif from the prion protein (PrP). The ligands are
XX identified by binding assays with the peptide (A) or peptides containing
XX (A). The ligands are used for detecting prion proteins (or prions) in

CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jakob diseases (in
CC iatrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strausser-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is a peptide containing the PrP octapeptide A used
CC to isolate the ligands of the invention.

XX Sequence 16 AA:

Query Match 100.0%; Score 55; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGG 8
| | | | | | | |
DB 1 GWGPHGG 8

RESULT 5
AAU11856

ID AAU11856 standard; peptide; 16 AA.

XX AC AAU11856;

DT 26-MAR-2002 (first entry)

XX DE Prion protein, PrP, octapeptide motif containing peptide variant #1.

KW Prion protein; PrP; ligand: octapeptide motif; scrapie;
KW prion-associated disease; Creutzfeldt-Jakob disease;
KW Gerstmann-Strausser-Scheinker disease; fatal familial insomnia;
KW feline spongiform encephalopathy; bovine spongiform encephalopathy;
KW transmissible mink encephalopathy; exotic ungulate encephalopathy;
KW chronic wasting disease.

XX OS Mammalia.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "Gly is acetylated"

FT Modified-site 16 /note= "Gly is amidated"

XX FT

XX WO200177687-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US11150.

XX PR 05-APR-2000; 2000US-0543188.

XX PA (VITE-) VI TECHNOLOGIES INC.

XX PI Hammond DJ, Wiltshire VR, Carbonell R, Shen H;

XX DR WPI; 2002-061944/08.

XX PT New ligands for prion proteins, useful for detection or removal or

XX PR prions and for treating prion-associated diseases, recognize a specific

XX PS octapeptide motif -

XX PS Disclosure; Page 10; 47pp; English.

XX The invention relates to a ligand of less than 6 kD that binds to a
XX polypeptide containing the sequence GlyTyrGlyInPrOHISGlyGly (A) or an
XX analogue that is the retro-inverse isomer of (A). The sequence A is
XX an octapeptide motif from the prion protein (PrP). The ligands are
XX identified by binding assays with the peptide (A) or peptides containing
XX (A). The ligands are used for detecting prion proteins (or prions) in

CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jacob diseases (in
CC iatrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strausler-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is a peptide containing the PrP octapeptide A
CC (containing the octapeptide in a different permutation to that shown in
CC AA011825) used to isolate the ligands of the invention.

XX SQ Sequence 16 AA:

Query Match 100.0%; Score 55; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. NO. 0.038; Mismatches 0; Gaps 0;
Matches 8; Conservative 0; Indels 0;

OY 1 GNGQPHGG 8
11111111
5 GNGQPHGG 12

RESULT 6
AAR38026

ID AAR38026 standard; protein: 18 AA.

AC AAR38026;

XX 14-OCT-1993 (first entry)

DE Bovine prion protein region E #2.

KW Antigen; prion; protein; region; frame shift; repeat; mutation; PrPc;
KW FSA; FSB; subfragment; antibody; treatment; spongiform encephalopathy;
KW human; sheep; cattle; cellular binding; aggregation; mammal; scrapie;
KW immune system; PrPsc; ratio-inverso peptide; enzymatic degradation;
KW resistance.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "One or more residues or may be absent"

FT Misc-difference 2 /note= "May be absent"

FT Misc-difference 3 /note= "May be absent"

FT Misc-difference 4 /note= "May be absent"

FT Misc-difference 5 /note= "May be absent"

FT Misc-difference 14 /note= "May be absent"

FT Misc-difference 15 /note= "May be absent"

FT Misc-difference 16 /note= "May be absent"

FT Misc-difference 17 /note= "May be absent"

FT Misc-difference 18 /note= "May be absent"

XX W09311155-A.

XX 10-JUN-1993.

XX 03-DEC-1992; 92WO-GB02246.

XX 03-DEC-1991; 91GB-0025747.

XX 10-JUL-1992; 92GB-0014663.

XX (PROT-) PROTEUS MOLECULAR DESIGN LTD.

PI Fishleigh RV, Mee RP, Robson B;
XX WPI, 1993-196994/24.

XX New polypeptide(s) contg. antigenic site of prion protein -
XX useful for treatment and diagnosis of mammalian encephalopathies
XX e.g. Creutzfeldt-Jacob disease and kuru

XX PS Claim 23; Page 70; 82pp; English.

XX The sequences given in AAR38025-36 represent polypeptides derived from
XX an antigenic site, region E, of a prion protein. Prion proteins
XX comprise six regions of interest (A-F), and two related frame shift
XX peptides sequences caused by a repeating section in region E having
XX a nucleic acid coding sequence frame shift mutation of +1 (Fsa) or -1
XX (Fsb) (see also AAR38037-38). These peptides and antibodies raised
XX against these may be used to treat or prevent spongiform encephalopathy
XX in humans, sheep or cattle. They can be used to block cellular binding
XX and aggregation of prion proteins and to stimulate the mammalian immune
XX system. These peptides may be used to distinguish between the normal
XX form of prion protein (PrPc) and the scrapie-associated form (PrPsc).
XX These peptides may include rare or synthetic amino acids or a ratio-
XX inverse peptide modification to improve resistance to enzymatic
XX degradation.

XX SQ Sequence 18 AA:

Query Match 100.0%; Score 55; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. NO. 0.042; Mismatches 0; Gaps 0;
Matches 8; Conservative 0; Indels 0;

OY 1 GNGQPHGG 8
11111111
4 GNGQPHGG 11

RESULT 7
AAR38029

ID AAR38029 standard; protein: 18 AA.

AC AAR38029;

XX 14-OCT-1993 (first entry)

DE Ovine prion protein region E #2.

KW Antigen; prion; protein; region; frame shift; repeat; mutation; PrPc;
KW FSA; FSB; subfragment; antibody; treatment; spongiform encephalopathy;
KW human; sheep; cattle; cellular binding; aggregation; mammal; scrapie;
KW immune system; PrPsc; ratio-inverso peptide; enzymatic degradation;
KW resistance.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "One or more residues or may be absent"

FT Misc-difference 2 /note= "May be absent"

FT Misc-difference 3 /note= "May be absent"

FT Misc-difference 4 /note= "May be absent"

FT Misc-difference 5 /note= "May be absent"

FT Misc-difference 14 /note= "May be absent"

FT Misc-difference 15 /note= "May be absent"

FT Misc-difference 16 /note= "May be absent"

FT Misc-difference 17 /note= "May be absent"

FT Misc-difference 18 /note= "One or more residue or may be absent"

FT XX

PN WO9311155-A.

XX 10-JUN-1993.

PD 03-DEC-1992; 92WO-GB02246.

XX 03-DEC-1991; 91GB-0025747.

PR 10-JUL-1992; 92GB-0014663.

XX (PROT-) PROTEUS MOLECULAR DESIGN LTD.

XX Fishleigh RV, Mee RP, Robson B;

XX WPI: 1993-196994/24.

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XX Claim 23; Page 70-71; 82pp; English.

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CC system. These peptides may be used to distinguish between the normal

CC form of prion protein (PrPc) and the scrapie-associated form (PrPsc).

CC These peptides may include rare or synthetic amino acids or a ratio-

CC inverse peptide modification to improve resistance to enzymatic

CC degradation.

CC

SQ Sequence 18 AA:

QY Query Match 100.0%; Score 55; DB 14; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGQPHGG 8

|||||||

4 GWGQPHGG 11

RESULT 8

AAR38032

ID AAR38032 standard; protein; 18 AA.

XX

AC AAR38032;

XX

DT 14-OCT-1993 (first entry)

XX

DE Human prion protein region E #2.

XX

KW Antigen; prion; protein; region; frame shift; repeat; mutation; PrPc;

KW Fsa; Fsb; subfragment; antibody; treatment; spongiform encephalopathy;

KW human; sheep; cattle; cellular binding; aggregation; mammal; scrapie;

KW immune system; PrPsc; ratio-inverse peptide; enzymatic degradation;

KW resistance.

XX

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Misc-difference 1 /note= "One or more residues or may be absent"

FT Misc-difference 2 /note= "May be absent"

FT

FT Misc-difference 3 /note= "May be absent"

FT FT

FT Misc-difference 4 /note= "May be absent"

FT FT

FT Misc-difference 5 /note= "May be absent"

FT FT

FT Misc-difference 14 /note= "May be absent"

FT FT

FT Misc-difference 15 /note= "May be absent"

FT FT

FT Misc-difference 16 /note= "May be absent"

FT FT

FT Misc-difference 17 /note= "May be absent"

FT FT

FT Misc-difference 18 /note= "May be absent"

FT FT

PN WO9311155-A.

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XX Fishleigh RV, Mee RP, Robson B;

XX WPI: 1993-196994/24.

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PS e.g. Creutzfeldt-Jacob disease and kuru

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CC system. These peptides may be used to distinguish between the normal

CC form of prion protein (PrPc) and the scrapie-associated form (PrPsc).

CC These peptides may include rare or synthetic amino acids or a ratio-

CC inverse peptide modification to improve resistance to enzymatic

CC degradation.

CC

SQ Sequence 18 AA:

QY Query Match 100.0%; Score 55; DB 14; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGQPHGG 8

|||||||

4 GWGQPHGG 11

RESULT 9

AAR38035

ID AAR38035 standard; protein; 26 AA.

XX

AC AAR38035;

XX

DT 14-OCT-1993 (first entry)

XX

DE Prion protein region E #2.

Query Match	100.0%	Score 55:	DB 14:	Length 26:
Best Local Similarity	100.0%	Pred. No. 0.06:		
Matches 8:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY	1 GWCQPHGC 8			
DB	7 GWCQPHGC 14			
Sequence	26 AA:			
<p>The sequences given in AAR38025-36 represent polypeptides derived from an antigenic site, region E, of a prion protein. Prion proteins comprise six regions of interest (A-F), and two related frame shift peptides sequences caused by a repeating section in region E having a nucleic acid coding sequence frame shift mutation of +1 (Fsa) or -1 (Fsb) (see also AAR38037-38). These peptides and antibodies raised against these may be used to treat or prevent spongiform encephalopathy in humans, sheep or cattle. They can be used to block cellular binding and aggregation of prion proteins and to stimulate the mammalian immune system. These peptides may be used to distinguish between the normal form of prion protein (PrPc) and the scrapie-associated form (PrPsc). These peptides may include rare or synthetic amino acids or a ratio-inverso peptide modification to improve resistance to enzymatic degradation.</p>				
<p>Claim 24: Page 71: 82pp: English.</p>				
<p>The sequences given in AAR38025-36 represent polypeptides derived from an antigenic site, region E, of a prion protein. Prion proteins comprise six regions of interest (A-F), and two related frame shift peptides sequences caused by a repeating section in region E having a nucleic acid coding sequence frame shift mutation of +1 (Fsa) or -1 (Fsb) (see also AAR38037-38). These peptides and antibodies raised against these may be used to treat or prevent spongiform encephalopathy in humans, sheep or cattle. They can be used to block cellular binding and aggregation of prion proteins and to stimulate the mammalian immune system. These peptides may be used to distinguish between the normal form of prion protein (PrPc) and the scrapie-associated form (PrPsc). These peptides may include rare or synthetic amino acids or a ratio-inverso peptide modification to improve resistance to enzymatic degradation.</p>				
<p>Antigen: prion; protein: region; frame shift; repeat; mutation; PrPc; Fsa; Fsb; subfragment; antibody; treatment; spongiform encephalopathy; human; sheep; cattle; cellular binding; aggregation; mammal; scrapie; immune system; PrPsc; ratio-inverso peptide; enzymatic degradation; resistance.</p>				
<p>Synthetic.</p>				
<p>MO9311155-A.</p>				
<p>10-JUN-1993.</p>				
<p>03-DEC-1992: 92MO-GB02246.</p>				
<p>03-DEC-1991: 91GB-0025747.</p>				
<p>10-JUL-1992: 92GB-0014663.</p>				
<p>(PROT-) PROTEUS MOLECULAR DESIGN LTD.</p>				
<p>Fishleigh RV, Nee RP, Robson B:</p>				
<p>WPI: 1993-196994/24.</p>				
<p>New polypeptide(s) contg. antigenic site of prion protein - useful for treatment and diagnosis of mammalian encephalopathies e.g. Creutzfeldt-Jacob disease and Kuru</p>				

```

PD      22-APR-1999.
XX
PE      15-OCT-1997;    97DE-1045443.
XX
PR      15-OCT-1997;    97DE-1045443.
XX
PA      (HERZ/) HERZOG-MESMER A.
XX
PI      Kiselev OI, Mesmer AH, Scheller A;
XX
DR      WPI; 1999-255775/22.
XX
PT      Diagnostic polyclonal antiserum specific for prion protein -
PM      obtained by immunisation with metal-containing polypeptide
XX
PS      Disclosure: Page 4; 12pp; German.
XX
CC      This invention describes a novel process for producing a polyclonal
CC      antiserum against a human or animal prion protein (PrP) which can be
CC      used in immunoassays for detecting PrP's. The method comprises (a)
CC      selecting a polypeptide that has a length of at least 10 amino acids and
CC      has an amino acid sequence at least 70% homologous to that of human,
CC      bovine or murine PrP in a region of at least 10 consecutive amino acids
CC      (b) binding a metal to the polypeptide by reaction with a metal compound
CC      and (c) infecting the metal-containing polypeptide into a host animal,
CC      optionally together with adjuvants, to induce production of a polyclonal
CC      antiserum.
XX
SQ      Sequence    42 AA;
XX
Query Match          100.0%; Score 55; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0
OY      1 GWGQPHCG 8
DB      |||||
        4 GWGQPHCG 11
RESULT 11
AAW70280
ID      AAW70280 standard; peptide; 178 AA.
AC      AAW70280;
DT      06-NOV-1998 (first entry)
DE      Peptide sequences used to raise antibodies against prion protein.
XX
KW      Spinal cord; cattle; sheep; pig; bovine spongiform encephalopathy;
KM      BSE; scrapie; transmissible spongiform encephalopathy; TSE;
KN      immunological assay; scrapie prion protein; prpsc.
OS      Synthetic.
FX
FH      Key Location/Qualifiers
FT      Region 28..61
FT      /note= "Synthetic sequence used to raise antibody
FT      Region 90..128 against prpsc"
FT      /note= "Synthetic sequence used to raise antibody
FT      against prpsc"
PN      WO9835236-A2.
PD      13-AUG-1998.
XX
PF      06-FEB-1998;    98WO-IE00007.
XX
PR      01-MAY-1997;    97IE-0000325.
PR      06-FEB-1997;    97IE-0000081.
PR      24-MAR-1997;    97IE-0000228.
XX

```

PA (ENFER-) ENFER TECHNOLOGY LTD.
XX
PI O'Connor M;
XX
DR WPI; 1998-447377/38.
XX
PT Detecting pathogenic prion(s) in animal carcasses - by reaction with
PT specific labelled antibody; used to detect those carrying agents for
PT bovine spongiform encephalopathy and scrapie
XX
PS Claim 3; Page 23; 25pp; English.
XX
CC The invention claims to provide a method for detecting transmissible
CC spongiform encephalopathies (TSE) in animals and in animal carcasses.
CC The method comprises of an immunological assay whereby the animal test
CC sample is reacted with a labelled antibody against scrapie prion protein
CC (PrP^{Sc}) and the amount of bound labelled antibody is then detected. The
CC anti-PrP^{Sc} antibodies used in the assay are raised against fragments of
CC the present synthetic peptide shown. The peptide fragments preferred
CC by the inventors are shown in the features table. The method is claimed
CC to be useful when applied to samples, particularly a cross-section of
CC the spinal cord, from cattle, sheep and pig carcasses for detection of
CC bovine spongiform encephalopathy (BSE) or scrapie.
XX
SQ Sequence 178 AA;
XX
Query Match 100.0%; Score 55; DB 19; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GWGQPHGG 8
DB 77 GWGQPHGG 84
XX
RESULT 12
AAB07316
ID AAB07316 standard; protein; 208 AA.
XX
AC AAB07316;
XX
DT 17-OCT-2000 (first entry)
XX
DE Mouse prion protein sequence.
XX
DE Mouse prion protein sequence.
XX
KW Mouse; prion protein; transmissible spongiform encephalopathy;
KW bovine spongiform encephalopathy; BSE diagnosis; TSE; PrP.
XX
Mus sp.
XX
FH Key Location/Qualifiers
FH Region 37..68
FT /note="Repeat region consisting of tandem repeats
FT of repeat unit: PHGGGWGQ (AAB07319)"
FT Disulfide-bond 156..191
FT Modified-site 208
FT /note="C-terminal phospho-inositol glycolipid
FT membrane anchor (-GPI)"
XX
WO200029850-A1.
XX
PN 25-MAY-2000.
XX
PD 27-OCT-1999; 99WO-FI00897.
XX
PE 17-NOV-1998; 98FI-0002481.
XX
PR (WALL-) WALLAC OY.
XX (BBSR-) BBSRC OFFICE.
XX
PI Hope J, Barnard GJR, Birkett CR,
XX
PS WPI; 2000-387880/33.
XX

XX
PT Novel immunoassay for prion protein, used for the determination of
PT transmissible spongiform encephalopathies in bovines -
XX
PS Disclosure; Page 41-42; 50pp; English.
XX
CC The present sequence is the mouse prion protein (PrP) sequence.
CC Conversion of the normal cellular form of PrP into an aggregated,
CC insoluble isoform is implicated in the pathogenesis of transmissible
CC spongiform encephalopathies (TSEs). Examples of TSEs include Bovine
CC spongiform encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease
CC (CJD) and Gerstmann-Strausler-Sheinker syndrome (GSS). The concentration
CC of this protein in body fluid or tissue samples may be measured by an
CC assay of the present invention, in which a PrP epitope is captured by an
CC antibody, which is then detected. The presence of PrP indicates TSE. PrP
CC epitopes (AAB07320-B07326) are derived from the protease resistant core
CC of PrP that is occluded when the PrP is in an aggregated state.
XX
SQ Sequence 208 AA;
XX
Query Match 100.0%; Score 55; DB 21; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GWGQPHGG 8
DB 41 GWGQPHGG 48
XX
RESULT 13
AAB07318
ID AAB07318 standard; protein; 208 AA.
XX
AC AAB07318;
XX
DT 17-OCT-2000 (first entry)
XX
DE Human prion protein sequence.
XX
DE Human prion protein sequence.
XX
KW Human; prion protein; transmissible spongiform encephalopathy;
KW bovine spongiform encephalopathy; BSE diagnosis; TSE; PrP.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 29..69
FT /note="Repeat region consisting of tandem repeats
FT of repeat unit: PHGGGWGQ (AAB07319)"
FT Disulfide-bond 157..192
FT Modified-site 208
FT /note="C-terminal phospho-inositol glycolipid
FT membrane anchor (-GPI)"
XX
WO200029850-A1.
XX
PN 25-MAY-2000.
XX
PD 27-OCT-1999; 99WO-FI00897.
XX
PE 17-NOV-1998; 98FI-0002481.
XX
PR (WALL-) WALLAC OY.
XX (BBSR-) BBSRC OFFICE.
XX
PI Hope J, Barnard GJR, Birkett CR,
XX
PS WPI; 2000-387880/33.
XX
PT Novel immunoassay for prion protein, used for the determination of
PT transmissible spongiform encephalopathies in bovines -
XX
PS Disclosure; Page 43-44; 50pp; English.
XX

CC The present sequence is the human prion protein (Prp) sequence.
CC Conversion of the normal cellular form of Prp into an aggregated,
CC insoluble isoform is implicated in the pathogenesis of Transmissible
CC Spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine
CC Spongiform Encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease
CC (CJD) and Gerstmann-Strausler-Sheinker syndrome (GSS). The concentration
CC of this protein in body fluid or tissue samples may be measured by an
CC assay of the present invention, in which a Prp epitope is captured by an
CC antibody, which is then detected. The presence of Prp indicates TSE. Prp
CC epitopes (AAB07320-B07326) are derived from the protease resistant core
CC of Prp that is occluded when the Prp is in an aggregated state.

XX Sequence 208 AA:

Query Match 100.0%; Score 55; DB 21; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGDPHGG 8
|||||||
34 GWGDPHGG 41

RESULT 14

AAB07327 standard; protein: 208 AA.

XX AAB07327;

DT 17-OCT-2000 (first entry)

XX Mouse prion protein sequence.

XX Mouse; prion protein: transmissible spongiform encephalopathy;

KM bovine spongiform encephalopathy; TSE diagnosis; Prp.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 37..68 /note= "Repeat region consisting of tandem repeats

FT Disulfide-bond 156..191 of repeat unit: PHGGWGQ (AAB07319)"

FT Modified-site 208 /note= "C-terminal phospho-inositol glycolipid

FT membrane anchor (-GPI)"

XX WO200029849-A1.

XX 25-MAY-2000.

PF 27-OCT-1999; 99WO-FI00896.

PR 17-NOV-1998; 98FI-0002480.

XX (WALL-) WALLAC OY.

PA (BBSR-) BBSRC OFFICE.

PI Hope J, Barnard GJR, Birkett CR;

XX WPI; 2000-399778/34.

XX New immunoassay for prion protein, used for determination of

XX transmissible spongiform encephalopathies in mammals, comprises

XX specific capture antibody -

XX Disclosure: Page 41-42; 50pp; English.

XX The present sequence is the mouse prion protein (Prp) sequence.

XX Conversion of the normal cellular form of Prp into an aggregated,
XX insoluble isoform is implicated in the pathogenesis of Transmissible
XX Spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine
XX Spongiform Encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease

CC (CJD) and Gerstmann-Strausler-Sheinker syndrome (GSS). The concentration
CC of this protein in body fluid or tissue samples may be measured by an
CC assay of the present invention, in which a Prp epitope is captured by an
CC antibody, which is then detected. The presence of Prp indicates TSE. Prp
CC epitopes (AAB07320-B07326) are derived from the protease resistant core
CC of Prp that is occluded when the Prp is in an aggregated state.

XX Sequence 208 AA:

Query Match 100.0%; Score 55; DB 21; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGDPHGG 8
|||||||
DB 41 GWGDPHGG 48

RESULT 15

AAB07329 standard; protein: 208 AA.

XX AAB07329;

DT 17-OCT-2000 (first entry)

XX Human prion protein sequence.

XX Human; prion protein: transmissible spongiform encephalopathy;

KM bovine spongiform encephalopathy; TSE diagnosis; Prp.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 29..69 /note= "Repeat region consisting of tandem repeats

FT Disulfide-bond 157..192 of repeat unit: PHGGWGQ (AAB07319)"

FT Modified-site 208 /note= "C-terminal phospho-inositol glycolipid

FT membrane anchor (-GPI)"

XX WO200029849-A1.

XX 25-MAY-2000.

PF 27-OCT-1999; 99WO-FI00896.

PR 17-NOV-1998; 98FI-0002480.

XX (WALL-) WALLAC OY.

PA (BBSR-) BBSRC OFFICE.

PI Hope J, Barnard GJR, Birkett CR;

XX WPI; 2000-399778/34.

XX New immunoassay for prion protein, used for determination of

XX transmissible spongiform encephalopathies in mammals, comprises

XX specific capture antibody -

XX Disclosure: Page 43-44; 50pp; English.

XX The present sequence is the human prion protein (Prp) sequence.

XX Conversion of the normal cellular form of Prp into an aggregated,
XX insoluble isoform is implicated in the pathogenesis of Transmissible
XX Spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine
XX Spongiform Encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease

XX (CJD) and Gerstmann-Strausler-Sheinker syndrome (GSS). The concentration
XX of this protein in body fluid or tissue samples may be measured by an
XX assay of the present invention, in which a Prp epitope is captured by an
XX antibody, which is then detected. The presence of Prp indicates TSE. Prp
XX epitopes (AAB07320-B07326) are derived from the protease resistant core

CC of PRP that is occluded when the PRP is in an aggregated state.

XX Sequence 208 AA;

Query Match 100.0%; Score 55; DB 21; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.43;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNGOPHGG 8

DB 34 GNGOPHGG 41

Search completed: January 3, 2003, 15:28:34
Job time : 36.4545 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:00 : Search time 13.2727 Seconds
(without alignments)
57.944 Million cell updates/sec

Title: US-09-543-188a-1
Perfect score: 55
Sequence: 1 GWGQPHHG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	226	2 A53892	prion-related prot
2	55	100.0	232	2 S71041	major prion protei
3	55	100.0	239	2 S53633	major prion protei
4	55	100.0	241	2 S71056	major prion protei
5	55	100.0	241	2 S71048	major prion protei
6	55	100.0	245	2 S53627	major prion protei
7	55	100.0	245	2 S71045	major prion protei
8	55	100.0	252	2 I61848	major prion protei
9	55	100.0	252	2 S53634	major prion protei
10	55	100.0	252	2 S53631	major prion protei
11	55	100.0	252	2 JC6175	major prion protei
12	55	100.0	253	1 UJHU	prion protein - ra
13	55	100.0	253	2 I37032	major prion protei
14	55	100.0	253	2 I61847	major prion protei
15	55	100.0	253	2 S53635	major prion protei
16	55	100.0	253	2 I84423	prion protein - si
17	55	100.0	253	2 S53618	major prion protei
18	55	100.0	253	2 S53619	major prion protei
19	55	100.0	253	2 S53620	major prion protei
20	55	100.0	253	2 S71055	major prion protei
21	55	100.0	253	2 S53623	major prion protei
22	55	100.0	253	2 S53624	major prion protei
23	55	100.0	253	2 S53625	major prion protei
24	55	100.0	253	2 S53617	major prion protei
25	55	100.0	253	2 S53614	major prion protei
26	55	100.0	253	2 S53616	major prion protei
27	55	100.0	254	1 UJHYTH	major prion protei
28	55	100.0	254	2 A34759	major prion prp-sc
29	55	100.0	254	2 B34759	prion protein - Ch

30	55	100.0	254	2 A23544	major prion protei
31	55	100.0	256	2 JU0268	major prion protei
32	55	100.0	256	2 S37149	major prion protei
33	55	100.0	256	2 A54281	major prion protei
34	55	100.0	257	2 A23545	major prion protei
35	55	100.0	257	2 JU01900	major prion protei
36	55	100.0	260	2 S53629	major prion protei
37	55	100.0	264	2 S37137	prion protein - gr
38	55	100.0	264	2 A54330	major prion protei
39	43	78.2	381	2 A44323	pentaxin prpx prec
40	41	74.5	395	2 T08350	hypothetical prote
41	41	74.5	521	2 E64862	probable membrane
42	40	72.7	327	2 E87218	probable prephenat
43	40	72.7	1161	2 T45294	hypothetical prote
44	39	70.9	69	2 B89016	protein B0213.5 li
45	39	70.9	120	2 F86824	hypothetical prote

ALIGNMENTS

RESULT 1
A53892
prion-related protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 13-Aug-1999
C:Accession: A53892
R:Liao, Y.C.; Tokes, Z.; Lim, E.; Lackey, A.; Woo, C.H.; Button, J.D.; Clawson, G.A.
Lab. Invest. 57, 370-374, 1987
A:Title: Cloning of rat "prion-related protein" cDNA.
A:Reference number: A53892; MUID:88037055; PMID:2889848
A:Accession: A53892
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-226 <LIA>
A:Cross-references: GB:M20313; NID:g206391; PIDN:AAA1947.1; PID:g206392
C:Superfamily: major prion protein

Query Match 100.0%; Score 55; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GWGQPHHG 8
Db 36 GWGQPHHG 43

RESULT 2

major prion protein - black-handed spider monkey (fragment)
C:Species: Ateles geoffroyi (black-handed spider monkey)
C:Date: 27-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999
R:Schatzl, H.M.
A:Accession: S71041; S53630
submitted to the EMBL Data Library, April 1994
A:Reference number: S71041
A:Accession: S71041
A:Molecule type: DNA
A:Residues: 1-232 <SCH>
R:Schatzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
A:Title: Prion protein gene variation among primates.
A:Reference number: S53614; MUID:95139066; PMID:7837269
A:Accession: S53630
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-194, 'R', 196-231 <SCW>
A:Cross-references: EMBL:U06309
C:Superfamily: major prion protein
C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane

Query Match 100.0%; Score 55; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

OY 1 GWGOPHGC 8
|||||
Db 48 GWGOPHGC 55

RESULT 3

S53633

major prion protein - douroucoulli (fragment)

C:Species: Aotus trivirgatus (douroucoulli, night monkey)

C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999

C:Accession: S53633; S71042

R:Schatz, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.

J. Mol. Biol. 245, 362-374, 1995

A:Title: Prion protein gene variation among primates.

A:Reference number: S53633

A:Status: nucleic acid sequence not shown

A:Accession: S53632

A:Status: nucleic acid sequence not shown

A:Accession: S53627

A:Cross-references: EMBL:U08293

R:Schatz, H.M.

submitted to the EMBL Data Library, April 1994

A:Reference number: S71041

A:Accession: S71042

A:Molecule type: DNA

A:Residues: 1-202, 'E', 204-239 <SCW>

A:Cross-references: EMBL:U08293; NID:9474344; PIDN:AAC50082.1; PID:9474345

C:Superfamily: major prion protein

C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane pro

Query Match 100.0%; Score 55; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGOPHGC 8
|||||
Db 48 GWGOPHGC 55

RESULT 4

S71056

major prion protein - mandrill (fragment)

C:Species: Papio sphinx, Mandrillus sphinx (mandrill)

C:Date: 27-Oct-1996 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999

C:Accession: S71056; S53621

R:Schatz, H.M.

submitted to the EMBL Data Library, April 1994

A:Reference number: S71041

A:Accession: S71056

A:Molecule type: DNA

A:Residues: 1-241 <SCW>

A:Cross-references: EMBL:U08303; NID:9474364; PIDN:AAC50091.1; PID:9474365

R:Schatz, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.

J. Mol. Biol. 245, 362-374, 1995

A:Title: Prion protein gene variation among primates.

A:Reference number: S53614; MUID:95139066; PMID:7837269

A:Accession: S53621

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-203, 'R', 205-240 <SCW>

A:Cross-references: EMBL:U08303

C:Superfamily: major prion protein

C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane pro

Query Match 100.0%; Score 55; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGOPHGC 8
|||||

Db 49 GWGOPHGC 56

RESULT 5

S71048

major prion protein - Calliobus moloch (fragment)

C:Species: Calliobus moloch

C:Date: 27-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999

C:Accession: S71048; S53632

R:Schatz, H.M.

submitted to the EMBL Data Library, April 1994

A:Reference number: S71041

A:Accession: S71048

A:Molecule type: DNA

A:Residues: 1-241 <SCW>

A:Cross-references: EMBL:U08312; NID:9475585; PIDN:AAC50100.1; PID:9475586

R:Schatz, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.

J. Mol. Biol. 245, 362-374, 1995

A:Title: Prion protein gene variation among primates.

A:Reference number: S53614; MUID:95139066; PMID:7837269

A:Accession: S53632

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-203, 'R', 205-240 <SCW>

A:Cross-references: EMBL:U08312

C:Superfamily: major prion protein

C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane

Query Match 100.0%; Score 55; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGOPHGC 8
|||||
Db 57 GWGOPHGC 64

RESULT 6

S53627

major prion protein - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999

C:Accession: S53627; S71043

R:Schatz, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.

J. Mol. Biol. 245, 362-374, 1995

A:Title: Prion protein gene variation among primates.

A:Reference number: S53614; MUID:95139066; PMID:7837269

A:Accession: S53627

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-245 <SCW>

A:Cross-references: EMBL:U08291

R:Schatz, H.M.

submitted to the EMBL Data Library, April 1994

A:Reference number: S71041

A:Accession: S71043

A:Molecule type: DNA

A:Residues: 1-10, 'V', 12-202, 'E', 204-245 <SCW>

A:Cross-references: EMBL:U08291; NID:9474340; PIDN:AAC50080.1; PID:9474341

C:Superfamily: major prion protein

C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane

Query Match 100.0%; Score 55; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGOPHGC 8
|||||
Db 56 GWGOPHGC 63

RESULT 7

S71045

major prion protein - Cercopithecus diana
C:Species: Cercopithecus diana
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
C:Accession: S71045; S53628
R:Schatzl, H.M.
submitted to the EMBL Data Library, April 1994
A:Reference number: S71041
A:Accession: S71045
A:Molecule type: DNA
A:Residues: 1-245 <SCH>
A:Cross-references: EMBL:U08292; NID:q474342; PIDN:AAC50081.1; PID:q474343
R:Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
A:Title: Prion protein gene variation among primates.
A:Reference number: S53614; MUID:95139066; PMID:7837269
A:Accession: S53628
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 8-10,'L',12-202,'R',204-239 <SCW>
A:Cross-references: EMBL:U08292
C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane pro

Query Match 100.0%; Score 55; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 55 GWGQPHGG 63

RESULT 8
161848
major prion protein precursor - common squirrel monkey
C:Species: Saimiri sciureus (common squirrel monkey)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999
C:Accession: I61848
R:Cervenakova, L.; Brown, P.; Goldfarb, L.G.; Nagle, J.; Pettone, K.; Rubenstein, R.; D
Proc. Natl. Acad. Sci. U.S.A. 91, 12159-12162, 1994
A:Title: Infectious amyloid precursor gene sequences in primates used for experimental t
A:Reference number: I36907; MUID:95083661; PMID:7991600
A:Accession: I61848
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-252 <RES>
A:Cross-references: EMBL:U15165; NID:9595852; PIDN:AAA68636.1; PID:9595853
C:Superfamily: major prion protein

Query Match 100.0%; Score 55; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 55 GWGQPHGG 62

RESULT 9
553634
major prion protein - common marmoset
C:Species: Callithrix jacchus (common marmoset)
C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999
C:Accession: S53634; S71047
R:Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
A:Title: Prion protein gene variation among primates.
A:Reference number: S53614; MUID:95139066; PMID:7837269
A:Accession: S53634
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-252 <SCH>
A:Cross-references: EMBL:U08304

R:Schatzl, H.M.
submitted to the EMBL Data Library, April 1994
A:Reference number: S71041
A:Accession: S71047
A:Molecule type: DNA
A:Residues: 1-209,'E',211-252 <SCW>
A:Cross-references: EMBL:U08304; NID:q474366; PIDN:AAC50092.1; PID:q474367
C:Superfamily: major prion protein
C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane

Query Match 100.0%; Score 55; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 55 GWGQPHGG 62

RESULT 10
553631
major prion protein - brown capuchin
C:Species: Cebus apella (brown capuchin, black-capped capuchin)
C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999
C:Accession: S53631; S71044
R:Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
A:Title: Prion protein gene variation among primates.
A:Reference number: S53614; MUID:95139066; PMID:7837269
A:Accession: S53631
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-252 <SCH>
A:Cross-references: EMBL:U08295
R:Schatzl, H.M.
submitted to the EMBL Data Library, April 1994
A:Reference number: S71041
A:Accession: S71044
A:Molecule type: DNA
A:Residues: 1-209,'E',211-252 <SCW>
A:Cross-references: EMBL:U08295; NID:q474348; PIDN:AAC50084.1; PID:q474349
C:Superfamily: major prion protein
C:Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane

Query Match 100.0%; Score 55; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 55 GWGQPHGG 62

RESULT 11
JG6175
prion protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 13-Aug-1999
C:Accession: JG6175
R:Loftus, B.; Rogers, M.
Gene 184, 215-219, 1997
A:Title: Characterization of a prion protein (PrP) gene from rabbit: a species with a
A:Reference number: JG6175; MUID:97183665; PMID:9031631
A:Accession: JG6175
A:Molecule type: DNA
A:Residues: 1-252 <LOF>
A:Cross-references: GB:U08334; NID:q1490412; PIDN:AAC48697.1; PID:q1490413
C:Comment: This protein is a cellular protein, it is involved in the neurodegenerativ
C:Genetics:
A:Gene: PrP
C:Superfamily: major prion protein
C:Keywords: disulfide bond; prion

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Query Match          100.0%; Score 55; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GWCQPHGC 8
DB      56 GWCQPHGC 63

RESULT 12
UTHU
major prion protein precursor - human
N:Alternate names: 11k amyloid protein; 27-30k sialoglycoprotein; PRP 27-30; PRP 33-35C;
C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 12-Apr-1996 #text_change 16-Jun-2000
A:Accession: A24173; A40372; A05017; S14078; I54322; I68597; I58135; I59184; I79633; I79
R:Kretzschmar, H.A.; Stowring, L.E.; Westaway, D.; Studdiblane, W.H.; Prusiner, S.B.; De
DNA 5, 315-324, 1986
A:Title: Molecular cloning of a human prion protein cDNA.
A:Reference number: A24173; MUID:86300093; PMID:3755672
A:Accession: A24173
A:Molecule type: mRNA
A:Residues: 1-253 <KRE>
A:Cross-references: GB:M13899; NID:9190467; PIDN:AAA60182.1; PID:9190468
R:Puckett, C.; Concanon, P.; Casey, C.; Hood, L.
Am. J. Hum. Genet. 49, 320-329, 1991
A:Title: Genomic structure of the human prion protein gene.
A:Reference number: A40372; MUID:91328137; PMID:1678248
A:Accession: A40372
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-80, 89-253 <PUC>
A:Cross-references: GB:X83416; NID:9747846; PIDN:CAA58442.1; PID:9747847
A:Note: the deletion may be a polymorphism; the alternative deletion of 82-89 could not
R:Lisio, Y.C.J.; Lebo, R.V.; Clawson, G.A.; Smuckler, E.A.
Science 233, 364-367, 1986
A:Reference number: A05017; MUID:86261778; PMID:3014653
A:Accession: A05017
A:Molecule type: mRNA
A:Residues: 8-117, 119-253 <LIA>
A:Cross-references: GB:D00015; NID:9220015; PIDN:BMA0011.1; PID:9220016; GB:M13667; NID
R:Tagliavini, F.; Prelli, F.; Ghiso, J.; Bugiani, O.; Serban, D.; Prusiner, S.B.; Farlow
EMBO J. 10, 513-519, 1991
A:Title: Amyloid protein of Gerstmann-Straussler-Scheinker disease (Indiana kindred) is
A:Reference number: S14078; MUID:91160504; PMID:1672107
A:Accession: S14078
A:Molecule type: protein
A:Residues: 58-72, 'X', 74-76, 'XX', 79, 'XXX', 83-86, 111-128, 'V', 130-150 <TAG>
R:Gerlich, J.F.; Knopman, D.S.; List, J.F.; Olson, K.; Frey, W.H.
Mol. Genet. 1, 443-444, 1992
A:Title: Deletion in the prion protein gene in a demented patient.
A:Reference number: I54322; MUID:93250789; PMID:1363802
A:Accession: I54322
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 9-83, 92-240 <RES>
A:Cross-references: GB:M81929; NID:9190517; PIDN:AAB59442.1; PID:9190518
A:Accession: I68597
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 8-240 <RES>
A:Cross-references: GB:M81930; NID:9190519; PIDN:AAB59443.1; PID:9190520
R:Brown, P.; Goldfarb, L.G.; McComble, W.R.; Nieto, A.; Squillacote, D.; Sheremata, W.;
Neurology 42, 422-427, 1992
A:Title: Atypical Creutzfeldt-Jakob disease in an American family with an insert mutatio
A:Reference number: I58135; MUID:92140671; PMID:1736177
A:Accession: I58135
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 51-91, 'PHCGGCGPHGCGGCGPHGCGGCGPHGCGGCGPHGCGGCGPHGCGGCGPHGCGGCGPHGCGGCG' <RE2>
A:Cross-references: GB:S80539; NID:9244698; PIDN:AAB21354.1; PID:9244699
R:Goldfarb, L.G.; Brown, P.; McComble, W.R.; Goldgaber, D.; Swergold, G.D.; Wills, P.R.;
Proc. Natl. Acad. Sci. U.S.A. 88, 10926-10930, 1991

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A:Title: Transmissible familial Creutzfeldt-Jakob disease associated with five, seven
A:Reference number: I59184; MUID:92073400; PMID:1683708
A:Accession: I59184
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 60-67 <GOL>
A:Cross-references: GB:S71208; NID:9239877; PIDN:AAB20521.1; PID:9239878; GB:S71210;
C:Genetics:
A:Gene: GDB:PRNP; CJD; PRIP
A:Cross-references: GDB:120720; OMIM:176640; OMIM:137440
A:Map position: 20pter-20p12
A:Introns: #status absent
A:Note: one intron occurs before the initiator codon
C:Note: this gene is associated with Creutzfeldt-Jakob disease (CJD), Gerstmann-Straus
C:Superfamily: major prion protein
C:Keywords: amyloid; blocked carboxyl end; brain; glycoprotein; lipoprotein; phosphat
F:11-22/Domain: signal sequence #status predicted <SIG>
F:23-230/Product: major prion protein #status predicted <MAT>
F:54-92/Region: 8-residue repeats (P-H-G-G-G-W-G-Q)
F:112-134/Domain: transmembrane #status predicted <TM1>
F:231-253/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:179-214/Disulfide bonds: #status predicted
F:181,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:230/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature f
Query Match          100.0%; Score 55; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GWCQPHGC 8
DB      56 GWCQPHGC 63

RESULT 13
major prion protein precursor - gorilla
C:Species: Gorilla gorilla (gorilla)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999
A:Accession: I37032
R:Cervenakova, L.; Brown, P.; Goldfarb, L.G.; Nagle, J.; Pettrone, K.; Rubenstein, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 12159-12162, 1994
A:Title: Infectious amyloid precursor gene sequences in primates used for experimenta
A:Reference number: I36907; MUID:95083661; PMID:7991600
A:Accession: I37032
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-253 <RES>
A:Cross-references: EMBL:U15166; NID:9563208; PIDN:AAA68633.1; PID:9563209
C:Superfamily: major prion protein_
Query Match          100.0%; Score 55; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GWCQPHGC 8
DB      56 GWCQPHGC 63

RESULT 14
major prion protein precursor - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999
A:Accession: I61847; S71060; S53615
R:Cervenakova, L.; Brown, P.; Goldfarb, L.G.; Nagle, J.; Pettrone, K.; Rubenstein, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 12159-12162, 1994
A:Title: Infectious amyloid precursor gene sequences in primates used for experimenta
A:Reference number: I36907; MUID:95083661; PMID:7991600
A:Accession: I61847
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

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A:Residues: 1-253 <RES>
 A:Cross-references: EMBL:U15039; NID:g609303; PIDN:AAA68632.1; PID:g609304
 R:Schaetzl, H.M.
 submitted to the EMBL Data Library, April 1994
 A:Reference number: S71041
 A:Accession: S71060
 A:Molecule type: DNA
 A:Residues: 1-253 <SCW>
 A:Cross-references: EMBL:U08296; NID:g474350; PIDN:AAC50085.1; PID:g474351
 R:Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
 J. Mol. Biol. 245, 362-374, 1995
 A:Title: Prion protein gene variation among primates.
 A:Reference number: S53614; MUID:95139066; PMID:7837269
 A:Accession: S53615
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-210, 'R', 212-253 <SCH>
 A:Cross-references: EMBL:U08296
 C:Superfamily: major prion protein
 Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane protein

Query Match 100.0%; Score 55; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.076;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNGOPHGG 8
 |||||
 Db 56 GNGOPHGG 63

RESULT 15
 S53635
 prion protein - simamang
 C:Species: Hylobates syndactylus (simamang)
 C:Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C:Accession: S53635
 R:Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
 J. Mol. Biol. 245, 362-374, 1995
 A:Title: Prion protein gene variation among primates.
 A:Reference number: S53614; MUID:95139066; PMID:7837269
 A:Accession: S53635
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-253 <SCH>
 A:Cross-references: EMBL:U08308; NID:g474374; PIDN:AAC50096.1; PID:g474375
 A:Note: the source was designated as Symphalangus syndactylus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
 Superfamily: major prion protein

Query Match 100.0%; Score 55; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.076;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNGOPHGG 8
 |||||
 Db 56 GNGOPHGG 63

Search completed: January 3, 2003, 15:33:13
 Job time : 13.2727 secs

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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:22:10 : Search time 6.90809 Seconds
(without alignments)
48,025 Million cell updates/sec

Title: US-09-543-188a-1
Perfect score: 55
Sequence: 1 GWCOPHC8 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	55	100.0	232	1	P40246 atelea geof
2	55	100.0	238	1	P95145 cercocebus
3	55	100.0	238	1	P95270 thetopithec
4	55	100.0	239	1	P40245 aotus triu
5	55	100.0	241	1	P40248 calliebus
6	55	100.0	241	1	P40255 mandrillus
7	55	100.0	245	1	P40250 cercopithec
8	55	100.0	246	1	P95172 cercopithec
9	55	100.0	246	1	P40250 cercopithec
10	55	100.0	246	1	P95176 cercocebus
11	55	100.0	252	1	P51446 atelea pani
12	55	100.0	252	1	P40247 callithrix
13	55	100.0	252	1	P40249 cebus apell
14	55	100.0	252	1	P95221 oryctolagus
15	55	100.0	253	1	P40251 colobus gue
16	55	100.0	253	1	P40252 gorilla gor
17	55	100.0	253	1	P04156 homo sapien
18	55	100.0	253	1	P40254 macaca fasc
19	55	100.0	253	1	P40253 pan troglod
20	55	100.0	253	1	P40256 pongo pygma
21	55	100.0	253	1	P40257 presbytis f
22	55	100.0	254	1	P060506 cricetus
23	55	100.0	254	1	P060468 cricetus
24	55	100.0	254	1	P04273 mesocricetu
25	55	100.0	254	1	P049255 mus musculu
26	55	100.0	254	1	P13852 rattus norv
27	55	100.0	254	1	P092073 simodon hi
28	55	100.0	255	1	P79141 camelus dro
29	55	100.0	255	1	P46501 canis famli
30	55	100.0	256	1	P53113 capra hircu
31	55	100.0	256	1	P79142 cervus elap
32	55	100.0	256	1	P018754 felis silve
33	55	100.0	256	1	P47852 odocolleus

34	55	100.0	256	1	P40246 atelea geof	P23907 ovis aries
35	55	100.0	256	1	P95145 cercocebus	O01880 bos taurus
36	55	100.0	256	1	P95270 thetopithec	P40243 tragelaphus
37	55	100.0	257	1	P40245 aotus triu	P52114 mustela put
38	55	100.0	257	1	P40248 calliebus	P40244 mustela vis
39	55	100.0	257	1	P40255 mandrillus	P49927 sus scrofa
40	55	100.0	260	1	P40250 cercopithec	P40258 saimiri sci
41	55	100.0	264	1	P95221 oryctolagus	P10279 bos taurus
42	55	100.0	264	1	P40251 colobus gue	P40242 tragelaphus
43	49	89.1	259	1	P40252 gorilla gor	P51780 tichosturus
44	43	78.2	381	1	P04156 homo sapien	P26022 homo sapien
45	41	74.5	507	1	P40254 macaca fasc	P75995 escherichia

ALIGNMENTS

RESULT 1
P40246 atelea geof (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Major prion protein precursor (Prp) (Prp27-30) (Prp33-35c) (Fragment).
PRNP.
Atelaea geoffroyi (Black-handed spider monkey).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelea;
NCBI_TaxID=9509;
[1]
SEQUENCE FROM N.A.
MEDLINE=95139066; PubMed=7837269;
Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
"Prion protein gene variation among primates";
J. Mol. Biol. 245:362-374(1995).
- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
"RODS".
- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMAN-STRAUSSLER SYNDROME
(GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
- SIMILARITY: BELONGS TO THE PRION FAMILY.

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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@sib-sib.ch).

EMBL: U08309; AAC50097.1; -
HSP: P04156; IEIG.
InterPro: IPR00817; Prion.
DR Pfam: PF00377; prion.1.
DR SMART: SM00157; PRP.1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 214
FT PROPEP 215 >232
FT LIPID 214 214
FT DISSULFID 163 198
FT CARBOHYD 165 195
FT CARBOHYD 181 181
FT DOMAIN 44 84
4 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-

FT	REPEAT	44	51	0.
FT	REPEAT	52	59	1.
FT	REPEAT	60	67	2.
FT	REPEAT	68	75	3.
FT	REPEAT	75		4.
FT	NON_TER	232		
EQ	SEQUENCE	232	232	
		AA:	25596	MM:
				0E2D75F04C05C4A CRC64;

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Query Match      100.0%; Score 55; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY      1  GWGQPHGG  8
          |||||
db      48  GWGQPHGG  55

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RESULT 2
PRIO_CERAT          STANDARD:      PRT:       238 AA.
095145; 095200;
01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).
GN Prnp.
OS Cercocebus atefrilmus, and
OC Macaca sylvanus (Barbary ape),
OC Euhariyola Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercocebus.
NCBI_taxid=36222, 9546;
[1]
RN SEQUENCE FROM N.A.
RP der Kuyil A.C., Dekker J.T., Goudsmat J.;
RA Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
RL -1 FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1 SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1 SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1 DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GESTAMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), ETC.
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1 SIMILARITY: BELONGS TO THE PRION FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: U75384; AAB50623.1; -.
DR EMBL: U75382; AAB50629.1; -.
DR HSSP: P0A925; IAC2.
DR InterPro: IPRO00817; Prion.
DR Pfam: PF00377; Prion.1.
DR SMART: SMO0157; PrP.1.
DR PROSITE: PS00291; Prion.1; 1.
DR PROSITE: PS00706; Prion.2; 1.
KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT NON_TER          1
FT SIGNAL            1
FT CHAIN             16 215
FT PROPSEP           216 238
FT LIPID              215 235
FT DISULFID           164 199
FT CARBOHYD           166 166
FT CATABOND           182 182
FT CARBOHYD           182 182
FT N-LINKED (GLCANAC. . . ) (POTENTIAL).
FT N-LINKED (GLCANAC. . . ) (POTENTIAL).

```

FT	DOMAIN	44	76	4	X	8	AA	TANDEM	REPEATS	OF	P-H-G-G-G-W-G
FT	REPEAT	44	52	1.							
FT	REPEAT	53	60	2.							
FT	REPEAT	61	68	3.							
FT	REPEAT	69	76	4.							
SEQ	SEQUENCE	238 AA;	26123 MM;	5F59A3EBEC3E3531B	CRC64;						

Query Match	100.0%	Score 55;	DB 1;	Length 238;
Best Local Similarity	100.0%	Prod. No. 0.041;		
Matches	8;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	1	GWGQPHGG	8	
Db	49	GWGQPHGG	56	

	RESULT	3
PRIOTHEGE		
ID PRIOTHEGE	STANDARD:	PRT; 238 AA.
AC Q95270;		
DT 01-NOV-1997 (Rel. 35, Created)		
DT 01-NOV-1997 (Rel. 35, Last sequence update)		
DT 01-NOV-1997 (Rel. 35, Last annotation update)		
DE Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).		
CN RMP OR PIP.		
OS Theropithecus gelada (Gelada baboon).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC Carcophiliaceae; Theropithecus.		
OX NCBI_TaxID=9565;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA der Kuyil A.C., Dekker J.T., Goudsmits J.;		
RL Submitted (NOV-1996) to the EMBL/Genbank/DDBJ databases.		
CC -I- EDUCATION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE		
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.		
CC -I- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED		
CC "RDS".		
CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.		
CC -I- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND		
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASE KRU,		
CC CEUTZFELDT-TAKOB DISEASE (CTD), GERSTMANN-STRAUSSLER SYNDROME		
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),		
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.		
CC -I- SIMILARITY: BELONGS TO THE PRION FAMILY.		

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CC or send an email to license@isb-sib.ch).		

DR EMBL: U75383; AAB50630.1; .		
DR HSPD: P04925; IAG2		
DR InterPro: IPRO00817; Prion.		
DR Pfam: PF00377; Prion; 1.		
DR SMART: SMO0157; PrP; 1.		
DR PROSITE: PS00291; PRION_1; 1.		
DR PROSITE: PS00706; PRION_2; 1.		
KW Prion; Brnln; Glycoprotein; GPI-anchor; Repeat; Signal.		
FT NON TER 1 1		
FT SIGNAL <1 15		
FT CHAIN 16 >238		
FT DISULFID 164 199		
FT CARBOHYD 166 166		
FT CARBOHYD 182 182		
FT DOMAIN 44 83		
FT FT O.		
REPEAT 44 52		
FT REPEAT 53 60		
FT FT 2.		

FT REPEAT 61 68 3.
FT REPEAT 69 76 4.
FT NON_TER 238
SQ SEQUENCE 238 AA; 26104 MW; 5F59BFF602243HDB CRC64;

Query Match
Best local Similarity 100.0%; Score 55; DB 1; Length 238;
Pred. No. 0.041;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGPHGG 8
Db 49 GWGPHGG 56

RESULT 4

PRIO_AOTTR
ID PRIO_AOTTR STANDARD: PRT; 239 AA.
AC P40245;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).
GN PRNP.
OS Aotus trivirgatus (Night monkey) (Douroucouli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95139066; PubMed=7837269;
RA Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
RT "Prion protein gene variation among primates."
RL J. Mol. Biol. 245:362-374(1995).
CC -!- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -!- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CRETZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -!- SIMILARITY: BELONGS TO THE PRION FAMILY.

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CC EMBL: U08293; AAC50082.1; -.
CC HSSP: P04925; IAG2.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; prion.1.
DR SMART: SM00157; PRP.1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 >239
FT DISULFID 171 206
FT CARBOHYD 173 173
FT CARBOHYD 189 189
FT DOMAIN 44 83
FT REPEAT 44 51
FT REPEAT 52 59
FT REPEAT 60 67
FT REPEAT 68 75

FT REPEAT 76 83 5.
FT NON_TER 239
SQ SEQUENCE 239 AA; 26246 MW; 2EFB77E34B7024A CRC64;

Query Match
Best local Similarity 100.0%; Score 55; DB 1; Length 239;
Pred. No. 0.041;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGPHGG 8
Db 48 GWGPHGG 55

RESULT 5

PRIO_CALMO
ID PRIO_CALMO STANDARD: PRT; 241 AA.
AC P40248;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).
GN PRNP.
OS Callithecus moloch (Dusky titi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callithecinae;
OC Callithecus.
OX NCBI_TaxID=9523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95139066; PubMed=7837269;
RA Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
RT "Prion protein gene variation among primates."
RL J. Mol. Biol. 245:362-374(1995).
CC -!- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -!- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CRETZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -!- SIMILARITY: BELONGS TO THE PRION FAMILY.

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CC EMBL: U08312; AAC50100.1; -.
CC HSSP: P04925; IAG2.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; prion.1.
DR SMART: SM00157; PRP.1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 >241
FT DISULFID 172 207
FT CARBOHYD 174 174
FT CARBOHYD 190 190
FT DOMAIN 44 84
FT REPEAT 44 52
FT REPEAT 53 60
FT REPEAT 61 68
FT REPEAT 69 76

FT REPEAT 77 84 5.
FT NON_TER 241 241
SQ SEQUENCE 241 AA: 26373 MM: C6D2013BE7CAEC93 CRC64;
Query Match 100.0%; Score 55; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GWCOPHCG 8
Db 57 GWCOPHCG 64
RESULT 6
PRIO_MANSNP
ID PRIO_MANSNP STANDARD: PRT: 241 AA.
AC P40255;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).
PNNP
OS Mandillus sphinx (Mandill) (Papio sphinx).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Mandillus.
OX NCBI_Taxid=9561;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95139066; PubMed-7837269;
RA Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
RT "Prion protein gene variation among primates.";
RL J. Mol. Biol. 245:362-374(1995).
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC -----
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CC -----
CC EMBL: U08303; AAC50091.1; -;
CC HSSP: P04925; IAG2.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; prion; 1.
DR SMART: SM00157; prp; 1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
KW prion; Brain; Glycoprotein; GPI-anchor; Repeat; signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 223
FT PROPEP 224 >241
FT LIPID 223 223
FT DISULFID 172 207
FT CARBOHYD 174 174
FT CARBOHYD 190 190
FT DOMAIN 44 84
FT REPEAT 44 52
FT REPEAT 53 60
O.
1.
2.

FT REPEAT 61 68 3.
FT REPEAT 69 76 4.
FT REPEAT 77 84 5.
FT NON_TER 241 241
SQ SEQUENCE 241 AA: 26398 MM: E539D84E2E2B59DE CRC64;
Query Match 100.0%; Score 55; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GWCOPHCG 8
Db 49 GWCOPHCG 56
RESULT 7
PRIO_CERAE
ID PRIO_CERAE STANDARD: PRT: 245 AA.
AC P40250;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C).
PNNP.
OS Cercopithecus aethiops (Green monkey) (Grivet), and
OC Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_Taxid=9534, 36224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95139066; PubMed-7837269;
RA Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
RT "Prion protein gene variation among primates.";
RL J. Mol. Biol. 245:362-374(1995).
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC -----
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CC -----
CC EMBL: U08291; AAC50080.1; -;
CC HSSP: P04925; IAG2.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; prion; 1.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; prp; 1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
KW prion; Brain; Glycoprotein; GPI-anchor; Repeat; signal.
FT SIGNAL 1 22
FT CHAIN 23 222
FT PROPEP 223 245
FT LIPID 222 222
FT DISULFID 171 206
FT CARBOHYD 173 173
FT CARBOHYD 189 189
O.
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
MAJOR PRION PROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT DOMAIN 51 83 4 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
FT REPEAT 51 59 0.
FT REPEAT 60 67 1.
FT REPEAT 68 75 2.
FT REPEAT 76 83 3.
FT REPEAT 76 83 4.
SQ SEQUENCE 245 AA; 26885 MW; D582B58E2726C99A CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 1; Length 245;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGG 8
DB 56 GWGPHGG 63

RESULT 8
PRIO_CERMO STANDARD; PRT; 246 AA.
095172; 095173;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-OUL-1998 (Rel. 36, Last annotation update)
DE Major prion protein precursor (Prp) (Prp27-30) (Prp33-35C) (Fragment).
GN PRNP.
OS Cercopithecus mona, and
OC Cercopithecus neglectus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36226, 36227;
RN [1]
RP SEQUENCE FROM N.A.
RA der Kuyt A.C., Dekker J.T., Goudsmit J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
-----
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-----
DR EMBL: U75386; AAB50625.1; -
DR EMBL: U75387; AAB50626.1; -
DR HSSP: P04925; IAG2.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; prion; 1.
DR SMART: SM00157; PRP; 1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 223 MAJOR PRION PROTEIN.
FT PROPEP 224 246 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 223 223 GPI-ANCHOR (BY SIMILARITY).
FT DISULFID 172 207 BY SIMILARITY.
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
FT DOMAIN 44 84 5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
FT REPEAT 44 52 0.
FT REPEAT 53 60 1.
FT REPEAT 61 68 2.
FT REPEAT 69 76 3.
FT REPEAT 77 84 4.
FT REPEAT 77 84 5.
SQ SEQUENCE 246 AA; 26900 MW; 835D147CA2B4FDD3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 1; Length 246;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGG 8
DB 49 GWGPHGG 56

RESULT 9
PRIO_CERPA STANDARD; PRT; 246 AA.
095174;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DE Major prion protein precursor (Prp) (Prp27-30) (Prp33-35C) (Fragment).
GN PRNP.
OS Cercopithecus patas.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=27677;
RN [1]
RP SEQUENCE FROM N.A.
RA der Kuyt A.C., Dekker J.T., Goudsmit J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
-----
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CC or send an email to license@sib-sib.ch).
-----
DR EMBL: U75388; AAB50627.1; -
DR HSSP: P04925; IAG2.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; prion; 1.
DR SMART: SM00157; PRP; 1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 223 MAJOR PRION PROTEIN.
FT PROPEP 224 246 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 223 223 GPI-ANCHOR (BY SIMILARITY).
FT DISULFID 172 207 BY SIMILARITY.
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 44 84 5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
```

FT REPEAT 44 52 0.
FT REPEAT 1. 53 60 2.
FT REPEAT 61 68 3.
FT REPEAT 69 76 4.
FT REPEAT 77 84 5.
SQ SEQUENCE 246 AA: 26886 MW: D35D105BEC53108 CRC64;
Query Match 100.0%; Score 55; DB 1; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GWGQPHGG 8
Db 49 GWGQPHGG 56
RESULT 10
PRIO_CERTO STANDARD: PRT: 246 AA.
095176:
01-NOV-1997 (rel. 35, Created)
01-NOV-1997 (rel. 35, Last sequence update)
01-NOV-1997 (rel. 35, Last annotation update)
DE Major prion protein precursor (Prp) (Prp33-35C) (Fragment).
GN PRNP.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA der Kuyi A.C., Dekker J.T., Goudsmit J.;
RL Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CRETZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC -----
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CC -----
CC EMBL: U75385; AAB50628.1; -.
CC HSSP: P04925; IAC2.
CC InterPro: IPR000817; Prion.
CC Pfam: PF00377; prion.1.
CC SMART: SM00157; prp.1.
CC PROSITE: PS00291; PRION_1; 1.
CC PROSITE: PS00706; PRION_2; 1.
CC Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 223
FT PROPEP 224 246
FT LIPID 223 223
FT DISULFID 172 207
FT CARBOHYD 174 174
FT CAROHD 150 190
FT DOMAIN 44 84
Q. BY SIMILARITY.
MAJOR PRION PROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
Q.

FT REPEAT 44 52 1.
FT REPEAT 53 60 2.
FT REPEAT 61 68 3.
FT REPEAT 69 76 4.
FT REPEAT 77 84 5.
SQ SEQUENCE 246 AA: 26914 MW: F58679CBEC5ADC7 CRC64;
Query Match 100.0%; Score 55; DB 1; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GWGQPHGG 8
Db 49 GWGQPHGG 56
RESULT 11
PRIO_ATEPA STANDARD: PRT: 252 AA.
ID PRIO_ATEPA
AC P51446:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 01-OCT-1996 (rel. 34, Last annotation update)
DE Major prion protein precursor (Prp) (Prp33-35C).
GN PRNP.
OS Ateles paniscus (Black spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atellinae; Ateles.
OX NCBI_TaxID=9510;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=95083661; PubMed=7991500;
RA Cervenakova L., Brown P., Goldfarb L.G., Nagle J., Petrone K.,
RA Rubenstein R., Dubnick M., Gibbs C.J., Gajdusek D.C.;
RT "Infectious amyloid precursor gene sequences in primates used for
RT experimental transmission of human spongiform encephalopathy.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:12159-12162(1994).
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CRETZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U15164; AAB68634.1; -.
CC HSSP: P04156; IEIG.
CC InterPro: IPR000817; Prion.
CC Pfam: PF00377; prion.1.
CC PRINTS: PR00341; PRION.
CC SMART: SM00157; prp.1.
CC PROSITE: PS00291; PRION_1; 1.
CC PROSITE: PS00706; PRION_2; 1.
CC Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 229
FT PROPEP 230 252
FT LIPID 229 229
FT DISULFID 178 213
FT CARBOHYD 180 180
Q. BY SIMILARITY.
MAJOR PRION PROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 51 90 5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
FT REPEAT 51 58 1.
FT REPEAT 59 66 2.
FT REPEAT 67 74 3.
FT REPEAT 75 82 4.
FT REPEAT 83 90 5.
SQ SEQUENCE 252 AA; 27718 MW; 20EA38A42DC56D1 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGPHGG 8
Db 55 GWGPHGG 62

MULT 12
PRIO_CALJA STANDARD: PRT: 252 AA.
AC P40247;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C).
GN PRNP.
OS Callitrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callitrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95139066; PubMed=7837269;
RA Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
RT "Prion protein gene variation among primates.";
RL J. Mol. Biol. 245:362-374(1995).
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMAN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U08304; AAC50092.1; -.
CC HSSP: P04925; 1AG2.
CC InterPro: IPR000817; Prion.
CC Pfam: PF00377; prion.1.
CC PRINTS: PR00341; PRION.
CC SMART: SM00157; PRP.1.
CC PROSITE: PS00291; PRION_1; 1.
CC PROSITE: PS00706; PRION_2; 1.
CC Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 229 BY SIMILARITY.
FT PROPEP 230 252 MAJOR PRION PROTEIN.
FT LIPID 229 229 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DISULFID 178 213 BY SIMILARITY.
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FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 51 90 5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
FT REPEAT 51 58 1.
FT REPEAT 59 66 2.
FT REPEAT 67 74 3.
FT REPEAT 75 82 4.
FT REPEAT 83 90 5.
SQ SEQUENCE 252 AA; 27639 MW; B2800B60FD5CE664 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGPHGG 8
Db 55 GWGPHGG 62

RESULT 13
PRIO_CEBAP STANDARD: PRT: 252 AA.
AC P40249;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C).
GN PRNP.
OS Cebus apella (Brown-capped capuchin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
OX NCBI_TaxID=9515;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95139066; PubMed=7837269;
RA Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
RT "Prion protein gene variation among primates.";
RL J. Mol. Biol. 245:362-374(1995).
CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMAN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U08295; AAC50084.1; -.
CC HSSP: P04156; 1E1G.
CC InterPro: IPR000817; Prion.
CC Pfam: PF00377; prion.1.
CC PRINTS: PR00341; PRION.
CC SMART: SM00157; PRP.1.
CC PROSITE: PS00291; PRION_1; 1.
CC PROSITE: PS00706; PRION_2; 1.
CC Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 229 BY SIMILARITY.
FT PROPEP 230 252 MAJOR PRION PROTEIN.
FT LIPID 229 229 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DISULFID 178 213 BY SIMILARITY.
```

FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 51 90 5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
 FT REPEAT 51 58 0.
 FT REPEAT 59 66 1.
 FT REPEAT 67 74 2.
 FT REPEAT 75 82 3.
 FT REPEAT 83 90 4.
 SQ SEQUENCE 252 AA; 27579 MW; A2DFCA0AD26D7821 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGQPHGG 8
 DB 55 GWGQPHGG 62

RESULT 14

PRO_RABIT STANDARD; PRT; 252 AA.
 AC Q95211;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Major prion protein precursor (Prp) (Prp27-30) (Prp33-35C).
 GN PRP OR PRP.
 OS Orctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-New Zealand white;
 RX MEDLINE=9718365; PubMed=9031631;
 RA Loftus B., Rogers M.;
 RT "Characterization of a prion protein (Prp) gene from rabbit: a
 RT species with apparent resistance to infection by prions.";
 RL Gene 184:215-219(1997).
 CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
 CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
 CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
 CC "RODS".
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
 CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
 CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMAN-STRAUSSLER SYNDROME
 CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
 CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
 CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
 CC
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 CC
 CC EMBL: U28334; AAC48697.1; -
 CC HSSP: P10279; IDWY.
 CC InterPro: IPR000817; Prion.
 CC Pfam: PF00377; Prion.1.
 CC PRINTS: PR00341; Prion.
 CC SMART: SM00157; Prp.1.
 CC PROSITE: PS00291; PRION_1; 1.
 CC PROSITE: PS00706; PRION_2; 1.
 KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 252 MAJOR PRION PROTEIN.
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 178 213 BY SIMILARITY.
 FT DOMAIN 51 92 5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
 FT REPEAT 51 59 0.
 FT REPEAT 60 67 1.
 FT REPEAT 68 75 2.
 FT REPEAT 76 83 3.
 FT REPEAT 84 92 4.
 SQ SEQUENCE 252 AA; 27432 MW; 2E177AAF38B23A54 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGQPHGG 8
 DB 56 GWGQPHGG 63

RESULT 15

PRO_COLGU STANDARD; PRT; 253 AA.
 AC P40251;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Major prion protein precursor (Prp) (Prp27-30) (Prp33-35C).
 GN PRP.
 OS Colobus guereza (Black-and-white colobus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Colobus.
 OX NCBI_TaxID=33548;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95139066; PubMed=7837269;
 RA Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.B.;
 RT "Prion protein gene variation among primates.";
 RL J. Mol. Biol. 245:362-374(1995).
 RN [2]
 RP SEQUENCE OF 8-253 FROM N.A.
 RA der Kuyt A.C., Dekker J.T., Goudsmit J.;
 RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
 CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
 CC -1- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
 CC "RODS".
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND
 CC ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU,
 CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMAN-STRAUSSLER SYNDROME
 CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
 CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
 CC -1- SIMILARITY: BELONGS TO THE PRION FAMILY.
 CC
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 CC
 CC EMBL: U08297; AAC50086.1; -
 CC EMBL: U75389; AAB50624.1; -
 CC HSSP: P04925; IAG2.
 CC InterPro: IPR000817; Prion.
 CC Pfam: PF00377; Prion.1.
 CC PRINTS: PR00341; Prion.
 CC SMART: SM00157; Prp.1.
 CC PROSITE: PS00291; PRION_1; 1.
 CC PROSITE: PS00706; PRION_2; 1.

KW Prion; Brain; Glycoprotein; GPI-anchor; Repeat; Signal.
 FT SIGNL 1 22 BY SIMILARITY.
 FT CHAIN 23 230 MAJOR PRION PROTEIN.
 FT PROPE 231 253 REMOVED IN MATURE FORM (BY SIMILARITY).
 FT LIPID 230 230 GPI-ANCHOR (BY SIMILARITY).
 FT DISULFID 179 214 BY SIMILARITY.
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 51 91 5 X 8 AA TANDEM REPEATS OF P-H-G-G-W-G-
 FT REPEAT 51 59 0.
 FT REPEAT 60 67 1.
 FT REPEAT 68 75 2.
 FT REPEAT 76 83 3.
 FT REPEAT 84 91 4.
 SQ SEQUENCE 253 AA; 27626 MW; 14B17477881F5316 CRC64; 5.

Query Match 100.0%; Score 55; DB 1; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWGQPHHG 8
 |||||
 Db 56 GWGQPHHG 63

Search completed: January 3, 2003, 15:29:18
 Job time : 7.90909 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2003, 15:24:35 ; Search time 27.0909 seconds
(without alignments)
60.846 Million cell updates/sec

Title: US-09-543-188a-1

Perfect score: 55

Sequence: 1 GWCGRHGG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	97	4	Q16409 homo sapien
2	55	100.0	105	6	Q97697 muntiacus m
3	55	100.0	117	11	Q9WUJ1 O9WUJ1
4	55	100.0	124	6	Q9TU20 varicia var
5	55	100.0	141	6	Q97905 tursiops tr
6	55	100.0	143	6	Q9M217 ovis aries
7	55	100.0	181	6	Q97911 budorcas ta
8	55	100.0	185	6	Q97694 cervus nip
9	55	100.0	195	6	Q97903 addax nasom
10	55	100.0	200	6	Q97693 canis lupus
11	55	100.0	202	6	Q97912 bison bonas
12	55	100.0	202	6	Q97908 capra nubia
13	55	100.0	202	6	Q97696 lama glama
14	55	100.0	204	6	Q97629 odocoileus
15	55	100.0	204	6	Q9TSI8 odocoileus
16	55	100.0	204	6	Q9TSI7 odocoileus

17	55	100.0	209	6	Q9TV02 camelus dro
18	55	100.0	211	6	Q77787 antilocapra
19	55	100.0	212	6	Q97698 cervus elap
20	55	100.0	213	6	Q9TV04 canis fami
21	55	100.0	214	6	Q9TV03 canis fami
22	55	100.0	215	6	Q97904 bos javanic
23	55	100.0	216	6	Q9TV00 bos taurus
24	55	100.0	220	6	Q92825 odocoileus
25	55	100.0	222	6	Q97913 equus quagg
26	55	100.0	223	6	Q97910 hippotragus
27	55	100.0	226	6	Q97907 gazella sub
28	55	100.0	227	6	Q97906 equus cabal
29	55	100.0	227	6	Q97909 tragelaphus
30	55	100.0	227	6	Q97964 equus cabal
31	55	100.0	233	4	P78446 homo sapien
32	55	100.0	235	6	Q97695 giraffa cam
33	55	100.0	240	11	Q8VHV4 microtus ag
34	55	100.0	243	11	P97895 mesocricetu
35	55	100.0	245	4	Q15216 homo sapien
36	55	100.0	245	6	Q9M2U7 mus musculu
37	55	100.0	246	4	Q60489 homo sapien
38	55	100.0	248	11	Q8VHV5 clethrionom
39	55	100.0	253	4	Q9UP19 homo sapien
40	55	100.0	253	4	Q96E70 homo sapien
41	55	100.0	253	4	Q8TRG0
42	55	100.0	253	11	Q9Z075 meriones un
43	55	100.0	254	6	Q9TSF8 oryctolagus
44	55	100.0	254	11	Q9Z0T4 sigmodon fu
45	55	100.0	254	11	Q9QY79 mus musculu

ALIGNMENTS

RESULT 1
ID 016409 PRELIMINARY: PRT: 97 AA.
AC Q16409; Q16407.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PPP amyloid (Prion protein) (Fragment).
GN PRNP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=92140671; PubMed=1736177;
RX Brown P., Goldfarb L.G., McCombie W.R., Nieto A., Squillacote D.,
RA Sheremata W., Little B.W., Godec M.S., Gibbs C.J., Jr., Gajdusek D.C.;
RT "Atypical Creutzfeldt-Jakob disease in an American family with an
RT insert mutation in the PRNP amyloid precursor gene."
RL Neurology 42:422-427(1992).
RN [2]
RP SEQUENCE OF 1-89 FROM N.A.
RX MEDLINE=96057178; PubMed=7572084;
RA Oda T., Kitamoto T., Tateishi J., Mitsuhashi T., Iwabuchi K., Haga C.,
RG Oguni E., Kato Y., Tomimaga I., Yanai K.;
RT "Prion disease with 144 base pair insertion in a Japanese family
RT line."
RL Acta Neuropathol. 90:80-86(1995).
RN [3]
RP SEQUENCE OF 1-81 FROM N.A.
RX MEDLINE=96390485; PubMed=8797471;
RA Cochran E.J., Bennett D.A., Cervenkova L., Kenney K., Bernard B.,
RA Foster N.L., Benson D.F., Goldfarb L.G., Brown P.;
RT "Familial Creutzfeldt-Jakob disease with a five-repeat octapeptide
RT insert mutation."
RL Neurology 47:727-733(1996).
DR EMBL: S80539; AAB21334.1; -;
DR EMBL: S79978; AAB35416.1; -;

DR EMBL: S83341; AAB50777.1; -.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion; 2.
DR PRINTS: PR00341; PRION.
KW Prion.
FT NON_TER 1 1
SQ SEQUENCE 97 AA; 9388 MW; D2A9F370DD10511D CRC64;

Query Match 100.0%; Score 55; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.079;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHCG 8
|||||
Db 46 GWGQPHCG 53

RESULT 2
097697

097697; PRELIMINARY; PRT; 105 AA.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Prion protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Prion protein (Fragment).
GN PrP.
OS Muntiacus muntjak (Muntjak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Muntiacinae; Muntiacus.
OX NCBI_TaxID=9888;
RN [1]
RP SEQUENCE FROM N.A.

01-MAY-1999 (TREMBlrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, Last sequence update)

01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Query Match 100.0%; Score 55; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHCG 8
|||||
Db 5 GWGQPHCG 12

RESULT 5
097905

097905; PRELIMINARY; PRT; 141 AA.

097905;

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DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).
GN PrP.
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Tursiops.
OC NCBI_TaxID=9739;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=PBL;
RX MEDLINE=99303687; PubMed=10373359;
RA Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
RA Schwarz T.F., Werner T., Schatzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PrPs reveals high conservation
RT of flexible regions of the prion protein."
RL J. Mol. Biol. 289:1163-1178(1999).
RL EMBL: AF117311; AAD19982.1; -
HSSP: P10279; IDMY.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; PRP. 1.
DR PROSITE: PS00291; PRION_1; 1.
FT NON_TER 1 1
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 15066 MW; 79BE306E2AAA187C CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 141;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GWGQPHGC 8
Db 36 GWGQPHGC 43

RESULT 6
O9M217 PRELIMINARY; PRT; 143 AA.
AC O9M217;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).
GN Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN (1)
RP SEQUENCE FROM N.A.
RA Herrmann L.M., Davis W.B., Li H., Wardrop J., Sy M.-S., Gambetti P.,
RA Knowles D.P.;
RT "Detection of PrPSc in peripheral blood mononuclear cells of scrapie
RT susceptible sheep."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF267507; AAF91403.1; -
HSSP: P10279; IDMY.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; PRP. 1.
DR PROSITE: PS00291; PRION_1; 1.
FT NON_TER 143 143
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 14428 MW; 4E2D296C6C8022E2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 143;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 GWGQPHGC 8
Db 59 GWGQPHGC 66

RESULT 7
O97911 PRELIMINARY; PRT; 181 AA.
AC O97911;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).
GN PrP.
OS Budorcas taxicolor (takín)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Budorcas.
OC NCBI_TaxID=37181;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=PBL;
RX MEDLINE=99303687; PubMed=10373359;
RA Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
RA Schwarz T.F., Werner T., Schatzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PrPs reveals high conservation
RT of flexible regions of the prion protein."
RL J. Mol. Biol. 289:1163-1178(1999).
RL EMBL: AF117326; AAD19997.1; -
HSSP: P10279; IDMY.
DR InterPro: IPR002395; Kininogen.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion.
DR PRINTS: PR00341; KININOGEN.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; PRP. 1.
DR PROSITE: PS00291; PRION_1; 1.
FT NON_TER 1 1
FT NON_TER 181 181
SQ SEQUENCE 181 AA; 19253 MW; A9001D086442E92A CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 181;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GWGQPHGC 8
Db 32 GWGQPHGC 39

RESULT 8
O97694 PRELIMINARY; PRT; 185 AA.
AC O97694;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).
GN PrP.
OS Cervus nippon dybowskii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OC NCBI_TaxID=88066;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97317556; PubMed=9174569;
RA Schatzl H.M., Wopfner F., Gilch S., von Brunn A., Jager G.,
RA "Is codon 129 of prion protein polymorphic in human beings but not in
RL animals?"
RL Lancet 349:1603-1604(1997).
RN (2)
RP SEQUENCE FROM N.A.
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RX MEDLINE=99303687; PubMed=10373359;
RA Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
Schwarz T.F., Werner T., Schatzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PRPs reveals high conservation
of flexible regions of the prion protein.";
RL J. Mol. Biol. 289:1163-1178(1999).
DR EMBL: AF113941; AAD13289.1; .
DR HSSP: P10279; IDWY.
DR InterPro: IPR002395; Kininogen.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion; 1.
DR PRINTS: PR00344; KININOEN.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; PRP; 1.
DR PROSITE: PS00291; PRION_1; 1.
FT NON_TER 1 1
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Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
DB 35 GWGPHHG 42

RESULT 9
O97903 PRELIMINARY; PRT; 195 AA.
ID O97903;
AC O97903;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).
GN PRP.
OS Addax nasomaculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Hippotraginae; Addax.
OX NCBI_TaxID=35915;
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RP SEQUENCE FROM N.A.
RC TISSUE=PBL.
RX MEDLINE=99303687; PubMed=10373359;
RA Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
Schwarz T.F., Werner T., Schatzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PRPs reveals high conservation
of flexible regions of the prion protein.";
RL J. Mol. Biol. 289:1163-1178(1999).
DR EMBL: AF117309; AAD19980.1; .
DR HSSP: P10279; IDWY.
DR InterPro: IPR002395; Kininogen.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion; 1.
DR PRINTS: PR00344; KININOEN.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; PRP; 1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
FT NON_TER 1 1
FT SEQUENCE 195 AA; 21331 MW; 6A9BA6A7E1AFCA9 CRC64;
SQ

Query Match 100.0%; Score 55; DB 6; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
DB 23 GWGPHHG 30

RESULT 10
O97693 PRELIMINARY; PRT; 195 AA.
ID O97693;
AC O97693;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Prion protein (Fragment).
GN PRP.
OS Canis lupus (Gray wolf).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9612;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303687; PubMed=10373359;
RA Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
Schwarz T.F., Werner T., Schatzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PRPs reveals high conservation
of flexible regions of the prion protein.";
RL J. Mol. Biol. 289:1163-1178(1999).
DR EMBL: AF113939; AAD12063.1; .
DR HSSP: P04925; IAG2.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion; 1.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; PRP; 1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
FT NON_TER 1 1
FT SEQUENCE 195 AA; 21097 MW; 9D18E4E9AA5D031 CRC64;
SQ

Query Match 100.0%; Score 55; DB 6; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
DB 18 GWGPHHG 25

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ID O97912;
AC O97912;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).
GN PRP.
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9902;
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RP SEQUENCE FROM N.A.
RC TISSUE=PBL.
RX MEDLINE=99303687; PubMed=10373359;
RA Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
Schwarz T.F., Werner T., Schatzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PRPs reveals high conservation
of flexible regions of the prion protein.";
RL J. Mol. Biol. 289:1163-1178(1999).
DR EMBL: AF117328; AAD19999.1; .
DR HSSP: P10279; IDWY.
DR InterPro: IPR002395; Kininogen.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion; 1.
DR PRINTS: PR00344; KININOEN.

DR PRINTS; PR00341; PRION.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00157; PRP; 1.
DR PROSITE; PS00291; PRION_1; 1.
DR PROSITE; PS00706; PRION_2; 1.
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FT NON_TER 200 200
SQ SEQUENCE 200 AA; 21674 MW; 1F270CDF4BE5271B CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 200;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
DB 16 GWGQPHGG 23

RESULT 12

O97908 PRELIMINARY; PRT; 202 AA.

DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).

OS Capra nubiana (Nubian ibex).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=72543;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=PBL;
RA MEDLINE=99303687; PubMed=10373359;
RA Mopfer F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
Schwarz T.F., Werner T., Scharzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PRPs reveals high conservation
of flexible regions of the prion protein.";
RL J. Mol. Biol. 289:1163-1178(1999).

DR EMBL; AF117319; AAD19990.1; -.
DR HSSP; P10279; IDWY.
DR InterPro; IPR002395; Kininogen.
DR InterPro; IPR000817; Prion.
DR Pfam; PF00377; prion.1.
DR PRINTS; PR00341; PRION.
DR PRINTS; PR00341; PRION.
DR SMART; SM00157; PRP; 1.
DR PROSITE; PS00291; PRION_1; 1.
DR PROSITE; PS00706; PRION_2; 1.
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FT NON_TER 202 202
SQ SEQUENCE 202 AA; 21949 MW; DB0634A43B4DB77F CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 202;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
DB 31 GWGQPHGG 38

RESULT 13

O97696 PRELIMINARY; PRT; 202 AA.

DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).

OS Lama glama (Llama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE=99303687; PubMed=10373359;
RA Mopfer F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,
Schwarz T.F., Werner T., Scharzl H.M.;
RT "Analysis of 27 mammalian and 9 avian PRPs reveals high conservation
of flexible regions of the prion protein.";
RL J. Mol. Biol. 289:1163-1178(1999).

DR EMBL; AF113943; AAD13291.1; -.
DR HSSP; P10279; IDWY.
DR InterPro; IPR000817; Prion.
DR Pfam; PF00377; prion.1.
DR PRINTS; PR00341; PRION.
DR SMART; SM00157; PRP; 1.
DR PROSITE; PS00291; PRION_1; 1.
DR PROSITE; PS00706; PRION_2; 1.
FT NON_TER 1 1
FT NON_TER 202 202
SQ SEQUENCE 202 AA; 21860 MW; FCA5232DB773F354 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 202;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
DB 11 GWGQPHGG 18

RESULT 14

O97629 PRELIMINARY; PRT; 204 AA.

DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Prion protein (Fragment).

OS Odocoileus virginianus (White-tailed deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoileinae; Odocoileus.
OX NCBI_TaxID=9874;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;
RA O'Rourke K.I., Miller M.W., Wild M.A., Williams E.S.;
RT "Prp alleles in free ranging and captive white tailed deer (Odocoileus
virginianus).";
RT Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF091558; AAC69626.1; -.
DR HSSP; P10279; IDWY.
DR InterPro; IPR002395; Kininogen.
DR InterPro; IPR000817; Prion.
DR Pfam; PF00377; prion.1.
DR PRINTS; PR00341; PRION.
DR PRINTS; PR00341; PRION.
DR SMART; SM00157; PRP; 1.
DR PROSITE; PS00291; PRION_1; 1.
DR PROSITE; PS00706; PRION_2; 1.
FT NON_TER 1 1
FT NON_TER 204 204
SQ SEQUENCE 204 AA; 22154 MW; CABA68F2B49C81E CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 204;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8

Db 36 GWGQPHG 43

RESULT 15

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AC 09TS18;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Prion protein (Fragment).
GN PRP.
OS Odocoleus virginianus (white-tailed deer).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoliinae; Odocolleus.
OX / NCBI_TaxID=9874;
RN [1]
SEQUENCE FROM N.A.

TISSUE-BRAIN;
O'Rourke K.I., Miller M.W., Wild M.A., Williams E.S.;
"Prp alleles in free ranging and captive white tailed deer (Odocoileus
virginianus).";
Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF091559; AAC69627.1; -
DR HSSP: P10279; IDWY.
DR InterPro: IPR000817; Prion.
DR Pfam: PF00377; Prion; 1.
DR PRINTS: PR00341; PRION.
DR SMART: SM00157; PRP; 1.
DR PROSITE: PS00291; PRION_1; 1.
DR PROSITE: PS00706; PRION_2; 1.
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Best Local Similarity 100.0%; Pred. NO. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHG 8
DB 36 GWGQPHG 43

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GenCore version 5.1.3
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OM protein - protein search, using sw model

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(without alignments)
19.615 Million cell updates/sec

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Perfect score: 55
Sequence: 1 GWGQPHGC 8

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	55	100.0	18	4	US-09-076-721-30
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14	55	100.0	253	1	US-08-692-892-2
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ALIGNMENTS

RESULT 1
US-08-244-701B-24
Sequence 24, Application US/08244/701B
Patent No. 3773572
GENERAL INFORMATION:
APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of prion proteins
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244, 701B
FILING DATE: 02-JUN-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
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OTHER INFORMATION: /note- "X may be absent or present independently
OTHER INFORMATION: of Y and denotes one or more amino acid(s)"
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LOCATION: 18

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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
Db 4 GWGPHHG 11

RESULT 2

US-08-244-701B-27
Sequence 27, Application US/08244701B
Patent No. 5773572

GENERAL INFORMATION:
APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of Prion Proteins
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,701B
FILING DATE: 02-JUN-1994
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
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Query Match 100.0%; Score 55; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
Db 4 GWGPHHG 11

RESULT 3
US-08-244-701B-30
Sequence 30, Application US/08244701B
Patent No. 5773572

GENERAL INFORMATION:
APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of Prion Proteins
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,701B
FILING DATE: 02-JUN-1994
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label-x
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US-08-244-701B-30

Query Match 100.0%; Score 55; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHHG 8
Db 4 GWGPHHG 11

RESULT 4
US-09-076-721-24
Sequence 24, Application US/09076721
Patent No. 6379905


```

: GENERAL INFORMATION:
: APPLICANT: Fishleigh, Robert V.
: APPLICANT: Robson, Barry
: APPLICANT: Mee, Roger P.
: TITLE OF INVENTION: Fragments of Prion Proteins
: NUMBER OF SEQUENCES: 67
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/076,721
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/244,701
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Fanucci, Allan A.
: REGISTRATION NUMBER: 30,256
: REFERENCE/DOCKET NUMBER: 8080-007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
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: Db 4 GWGQPHGC 11
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: RESULT 5
: US-09-076-721-27
: Sequence 27, Application US/09076721
: Patent No. 6379905
: GENERAL INFORMATION:
: APPLICANT: Fishleigh, Robert V.
: APPLICANT: Robson, Barry
: APPLICANT: Mee, Roger P.
: TITLE OF INVENTION: Fragments of Prion Proteins
: NUMBER OF SEQUENCES: 67
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
```

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: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/076,721
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/244,701
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Fanucci, Allan A.
: REGISTRATION NUMBER: 30,256
: REFERENCE/DOCKET NUMBER: 8080-007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 27:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
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: RESULT 6
: US-09-076-721-30
: Sequence 30, Application US/09076721
: Patent No. 6379905
: GENERAL INFORMATION:
: APPLICANT: Fishleigh, Robert V.
: APPLICANT: Robson, Barry
: APPLICANT: Mee, Roger P.
: TITLE OF INVENTION: Fragments of Prion Proteins
: NUMBER OF SEQUENCES: 67
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/076,721
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,701
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Panucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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RESULT 7
US-08-244-701B-46
Sequence 46, Application US/08244701B
Patent No. 5773572
GENERAL INFORMATION:
APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of Prion Proteins
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,701B
FILING DATE: 02-JUN-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Panucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-244-701B-46
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Db 7 GWGPHGG 14
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US-09-076-721-46
Sequence 46, Application US/09076721
Patent No. 6379905
GENERAL INFORMATION:
APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of Prion Proteins
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,721
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,701
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Panucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-076-721-46

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Best Local Similarity 100.0%; Pred. No. 0.024;
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Sequence 18, Application US/09128450
Patent No. 6211149

GENERAL INFORMATION:
APPLICANT: Chesebri, Bruce W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette

TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
FILE REFERENCE: 50121
CURRENT APPLICATION NUMBER: US/09/128,450

CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18

LENGTH: 208

TYPE: PRT
ORGANISM: Hamster sp.

FEATURE:

NAME/KEY: NON_TER
LOCATION: (1)..(2)

US-09-128-450-18

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RESULT 10

US-09-823-494-18

Sequence 18, Application US/09823494
Patent No. 6355610

GENERAL INFORMATION:

APPLICANT: Chesebri, Bruce W

APPLICANT: Caughey, Byron W

APPLICANT: Chabry, Joelle

APPLICANT: Priola, Susette

TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion

TITLE OF INVENTION: Protein

FILE REFERENCE: 50121
CURRENT APPLICATION NUMBER: US/09/823,494

CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/128,450

PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 208

TYPE: PRT

ORGANISM: Hamster sp.

FEATURE:

NAME/KEY: NON_TER

LOCATION: (1)..(2)

US-09-823-494-18

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DB 34 GWGQPHGG 41

RESULT 11

US-08-242-188-2

Sequence 2, Application US/08242188

Patent No. 5565186

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

APPLICANT: Scott, Michael R.

TITLE OF INVENTION: METHOD OF DETECTING PRIONS IN A SAMPLE

TITLE OF INVENTION: AND TRANSGENIC ANIMAL USED FOR SAME

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Karl Bosicevic

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA

COUNTRY: USA

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/242,188

FILING DATE: 13-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bosicevic, Karl

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 06510/014001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 854-5277

TELEFAX: (415) 854-0875

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: HUMAN PRION PROTEIN, HuPrP

US-08-242-188-2

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DB 56 GWGQPHGG 63

RESULT 12

US-08-509-261A-2

Sequence 2, Application US/08509261A

Patent No. 5763244

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.

APPLICANT: Scott, Michael R.

APPLICANT: Telling, Glenn

TITLE OF INVENTION: Method of Detecting Prions
TITLE OF INVENTION: in a Sample and Transgenic Animal Used fore

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/509,261A
FILING DATE: 31-JUL-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 6510-030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-509-261A-2

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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 56 GWGQPHGG 63

RESULT 13
US-08-660-626-8
Sequence 8, Application US/08660626
Patent No. 5789655
GENERAL INFORMATION:
APPLICANT: Stanley B. Prusiner
APPLICANT: Glenn C. Telling
APPLICANT: Fred E. Cohen
APPLICANT: Michael R. Scott
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
TITLE OF INVENTION: EPTROPE-TAGGED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Asctii
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,626
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Valela Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN PRION PROTEIN, HuPrP
US-08-660-626-8

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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 56 GWGQPHGG 63

RESULT 14
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Sequence 2, Application US/08692892
Patent No. 5792901
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Scott, Michael R.
APPLICANT: Telling, Glenn
TITLE OF INVENTION: DETECTING PRIONS IN A SAMPLE AND
TITLE OF INVENTION: PRION PREPARATION AND TRANSGENIC ANIMAL USED FOR SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Karl Bozicevic
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/692,892
FILING DATE: 30-JULY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/056001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN PRION PROTEIN, HuPrP
US-08-692-892-2

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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15

US-08-713-939A-2

; Sequence 2, Application US/08713939A

; Patent No. 3846533

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.

; APPLICANT: Williamson, R. Anthony

; APPLICANT: Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

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FILING DATE: 13-SEP-1996

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bozicevic, Karl

REGISTRATION NUMBER: 28,807

REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-5277

TELEFAX: 415-854-0875

TELEX:

INFORMATION FOR SEQ ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-713-939A-2

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Db 56 GWGQPHGG 63

Query Match 100.0%; Score 55; DB 2; Length 253;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.3
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Perfect score: 55
Sequence: 1 GMGQPHGG 8

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Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Minimum number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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7	55	100.0	254	9	US-10-106-574-6
8	55	100.0	254	9	US-10-106-574-7
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33	40	72.7	1239	9	US-10-007-747-52	Sequence 52, Appl
34	40	72.7	1244	9	US-09-945-901-46	Sequence 46, Appl
35	40	72.7	1244	9	US-10-007-747-46	Sequence 46, Appl
36	38	69.1	5179	9	US-10-025-380-1068	Sequence 1068, Ap
37	38	69.1	5179	10	US-09-922-217-1068	Sequence 1068, Ap
38	38	69.1	5179	10	US-09-833-263-1068	Sequence 1068, Ap
39	37	67.3	40	8	US-08-424-550B-552	Sequence 552, App
40	37	67.3	100	9	US-10-001-835-172	Sequence 172, App
41	37	67.3	242	10	US-09-764-853-609	Sequence 609, App
42	37	67.3	242	10	US-09-764-858-199	Sequence 199, App
43	37	67.3	677	10	US-09-006-298-21	Sequence 21, Appl
44	37	67.3	696	10	US-09-925-300-1253	Sequence 1253, Ap
45	36.5	66.4	67	10	US-09-864-761-44423	Sequence 44423, A

ALIGNMENTS

RESULT 1
US-09-939-780-2
; Sequence 2, Application US/09939780
; Patent No. US20020168689A1
; GENERAL INFORMATION:
; APPLICANT: O'Connor, Michael
; TITLE OF INVENTION: Immunological Assay for Spongiform Encephalopathies
; FILE REFERENCE: 500020US
; CURRENT APPLICATION NUMBER: US/09/939,780
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/147,761
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: PCT/IE98/00007
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: prion protein
US-09-939-780-2
Query Match 100.0%; Score 55; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 GMGQPHGG 22
QY 1 GMGQPHGG 8
|||||||
US-09-147-761-2
; Sequence 2, Application US/09147761
; Patent No. US20010010918A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOLOGICAL ASSAY FOR SPONGIFORM
; TITLE OF INVENTION: ENCEPHALOPATHIES

NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,761
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO IE/98/00007
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTINA GATES
REFERENCE/DOCKET NUMBER: PL678pct
TELECOMMUNICATION INFORMATION:
TELEPHONE: 353-1-6605033
TELEFAX: 353-1-6606920
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 43
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: amino acid
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM:
CELL TYPE:
US-09-147-761-2

Query Match 100.0%; Score 55; DB 10; Length 43;

Best Local Similarity 100.0%; Pred. No. 0.044; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWCQPHGG 8
|||||
DB 15 GWCQPHGG 22

RESULT 3
US-09-904-987-3
Sequence 3, Application US/09904987
Patent No. US20020037908A1
GENERAL INFORMATION:
APPLICANT: No. US20020037908A1acetyl, Inc.
TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepath
FILE REFERENCE: 42108/26146
CURRENT FILING DATE: 2001-07-12
CURRENT APPLICATION NUMBER: US/09/904,987
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 253
TYPE: PRT
ORGANISM: homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI ENTREZ / XM_009567
DATABASE ENTRY DATE: 2001-04-17
RELEVANT RESIDUES: (1)..(253)
US-09-904-987-3

Query Match 100.0%; Score 55; DB 10; Length 253;

Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWCQPHGG 8
|||||
DB 56 GWCQPHGG 63

RESULT 4

US-09-919-172-57
Sequence 57, Application US/09919172
Patent No. US20020119463A1
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 57
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020119463A1 1256895CD1
US-09-919-172-57

Query Match 100.0%; Score 55; DB 10; Length 253;

Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWCQPHGG 8
|||||
DB 56 GWCQPHGG 63

RESULT 5
US-09-943-906-2
Sequence 2, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-943-906-2

Query Match
Best Local Similarity 100.0%; Score 55; DB 9; Length 254;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 56 GWGQPHGG 63

RESULT 6
US-10-106-574-5
Sequence 5, Application US/10106574
Patent No. US20020164335A1
GENERAL INFORMATION:
APPLICANT: Harris, David A.
TITLE OF INVENTION: Compositions and Methods for the Study and Diagnosis of Prion Dis
FILE REFERENCE: 09789280.0003
CURRENT APPLICATION NUMBER: US/10/106,574
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 254
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-106-574-5

Query Match
Best Local Similarity 100.0%; Score 55; DB 9; Length 254;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 63 GWGQPHGG 70

RESULT 7
US-10-106-574-6
Sequence 6, Application US/10106574
Patent No. US20020164335A1
GENERAL INFORMATION:
APPLICANT: Harris, David A.
TITLE OF INVENTION: Compositions and Methods for the Study and Diagnosis of Prion Dis
FILE REFERENCE: 09789280.0003
CURRENT APPLICATION NUMBER: US/10/106,574
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 254
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-106-574-6

Query Match
Best Local Similarity 100.0%; Score 55; DB 9; Length 254;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 63 GWGQPHGG 70

RESULT 8
US-10-106-574-7

Sequence 7, Application US/10106574
Patent No. US20020164335A1
GENERAL INFORMATION:
APPLICANT: Harris, David A.
TITLE OF INVENTION: Compositions and Methods for the Study and Diagnosis of Prion
FILE REFERENCE: 09789280.0003
CURRENT APPLICATION NUMBER: US/10/106,574
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 254
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-106-574-7

Query Match
Best Local Similarity 100.0%; Score 55; DB 9; Length 254;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 63 GWGQPHGG 70

RESULT 9
US-10-106-574-8
Sequence 8, Application US/10106574
Patent No. US20020164335A1
GENERAL INFORMATION:
APPLICANT: Harris, David A.
TITLE OF INVENTION: Compositions and Methods for the Study and Diagnosis of Prion
FILE REFERENCE: 09789280.0003
CURRENT APPLICATION NUMBER: US/10/106,574
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 254
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-106-574-8

Query Match
Best Local Similarity 100.0%; Score 55; DB 9; Length 254;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGQPHGG 8
|||||
Db 63 GWGQPHGG 70

RESULT 10
US-09-943-906-1
Sequence 1, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-943-906-1

Query Match 100.0%; Score 55; DB 10; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGC 8
|||||||
Db 63 GWGPHGC 70

RESULT 11
US-09-943-906-4
Sequence 4, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875

TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-943-906-4

Query Match 100.0%; Score 55; DB 10; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGC 8
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Db 58 GWGPHGC 65

RESULT 12
US-10-109-551-2
Sequence 2, Application US/10109551
Publication No. US20020194635A1
GENERAL INFORMATION:
APPLICANT: DUNNE, PATRICK W.
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
FILE REFERENCE: TAMK:20705
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 256
TYPE: PrT
ORGANISM: Bos taurus
US-10-109-551-2

Query Match 100.0%; Score 55; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGC 8
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Db 59 GWGPHGC 66

RESULT 13
US-10-109-551-4
Sequence 4, Application US/10109551
Publication No. US20020194635A1
GENERAL INFORMATION:
APPLICANT: DUNNE, PATRICK W.
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
FILE REFERENCE: TAMK:20705
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 256
TYPE: PrT
ORGANISM: Ovis aries
US-10-109-551-4

Query Match 100.0%; Score 55; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGG 8
|||||
Db 59 GWGPHGG 66

RESULT 14
US-10-109-551-6
; Sequence 6, Application US/10109551
; Publication No. US20020194635A1
; GENERAL INFORMATION:
; APPLICANT: DUNNE, PATRICK W.
; APPLICANT: PIEDRAHITA, JORGE
; TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
; FILE REFERENCE: TARK:207US
; CURRENT APPLICATION NUMBER: US/10/109,551
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,549
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Odocolleus virginianus
US-10-109-551-6

Query Match 100.0%; Score 55; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGG 8
|||||
Db 59 GWGPHGG 66

RESULT 15
US-10-109-551-8
; Sequence 8, Application US/10109551
; Publication No. US20020194635A1
; GENERAL INFORMATION:
; APPLICANT: DUNNE, PATRICK W.
; APPLICANT: PIEDRAHITA, JORGE
; TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
; FILE REFERENCE: TARK:207US
; CURRENT APPLICATION NUMBER: US/10/109,551
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,549
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Odocolleus hemionus hemionus
US-10-109-551-8

Query Match 100.0%; Score 55; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GWGPHGG 8
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Db 59 GWGPHGG 66

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2003, 15:21:45 : Search time 26.5909 seconds
(without alignments)
30.067 Million cell updates/sec

Title: US-09-543-188a-3
Perfect score: 34
Sequence: 1 LLIWIP 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	6	23	AAU11826
2	34	100.0	87	22	ABB40848
3	34	100.0	87	22	ABB25012
4	34	100.0	87	22	AA61707
5	34	100.0	87	22	AA674503
6	34	100.0	87	22	AA634616
7	34	100.0	87	23	ABG44369
8	34	100.0	269	21	ABB26446
9	34	100.0	269	22	ABB68723
10	34	100.0	453	21	AA820922

11	34	100.0	554	22	AAU14133
12	34	100.0	754	23	ABB92828
13	33	97.1	298	20	AAV24023
14	33	97.1	301	20	AAV24022
15	32	94.1	128	15	AA853332
16	32	94.1	128	20	AAV28360
17	32	94.1	142	16	AA813111
18	32	94.1	177	22	AA815989
19	32	94.1	251	22	AAU33248
20	32	94.1	484	22	ABG05597
21	31	91.2	12	19	AAW60537
22	31	91.2	16	17	AA84070
23	31	91.2	20	12	AA810540
24	31	91.2	20	19	AAW69959
25	31	91.2	20	19	AAW68295
26	31	91.2	20	20	AAW17756
27	31	91.2	20	21	AAV52559
28	31	91.2	20	22	AAE11049
29	31	91.2	20	22	AAE08740
30	31	91.2	20	22	AAE04428
31	31	91.2	20	22	AAE01995
32	31	91.2	21	18	AAW12384
33	31	91.2	21	22	AA866331
34	31	91.2	21	23	AAU75372
35	31	91.2	21	23	AAU75379
36	31	91.2	42	22	AA871931
37	31	91.2	45	21	AA803863
38	31	91.2	47	23	AAW47704
39	31	91.2	65	21	AA824836
40	31	91.2	69	22	AAU21012
41	31	91.2	80	21	AAV52548
42	31	91.2	91	22	AAU14672
43	31	91.2	100	21	AAV64671
44	31	91.2	116	22	AAU44203
45	31	91.2	118	21	AAV52541

ALIGNMENTS

RESULT 1	
AAU11826	
ID	AAU11826 standard; peptide: 6 AA.
AC	AAU11826;
XX	
DT	26-MAR-2002 (first entry)
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DE	Peptide ligand for Prion protein, Prp, #1.
XX	
KW	Prion protein; Prp; ligand; octapeptide motif; scrapie;
KW	prion-associated disease; Creutzfeldt-Jakob disease;
KW	Gerstmann-Strausler-Scheinker disease; fatal familial insomnia;
KW	feline spongiform encephalopathy; bovine spongiform encephalopathy;
KW	transmissible mink encephalopathy; exotic ungulate encephalopathy;
XX	chronic wasting disease.
OS	Synthetic.
XX	
PN	WO200177687-A2.
XX	
PD	18-OCT-2001.
XX	
PF	05-APR-2001; 2001WO-US11150.
XX	
PR	05-APR-2000; 2000US-0543188.
XX	
PA	(VITE-) VI TECHNOLOGIES INC.
XX	
PI	Hammond DJ, Wiltshire VR, Carbonell R, Shen H;
XX	
DR	WPI; 2002-061944/08.
XX	

Human novel protei
Herbicide/activ
Human CMRF-35-H9 r
Human CMRF-35-H9 r
Human CMRF-35-H9 r
KM-603 light chain
Antibody light cha
Rat monoclonal ant
Human novel secret
Novel human secret
Novel human diago
Oligopeptide from
Plasmid pBlue-TH6
Eukaryotic signal
Ig kappa chain lea
Ig kappa chain lea
Target signal pept
Consensus murine I
Human Ig (immunog
Immunoglobulin kap
Human immunoglobul
Immunoglobulin (Ig
Murine Ig kappa-ch
Ig-kappa chain lea
Mouse kappa immuno
Mouse kappa immuno
Murine sig-mendof
Active human neuro
Fragment of a reco
Plant SDF encoded
Human novel foetal
Murine Ig-kappa si
Novel bone marrow
Human 5' EST relat
Protonlactetium
KappalAMP-Th fusio

PT New ligands for prion proteins, useful for detection or removal or
PT prions and for treating prion-associated diseases, recognize a specific
PT octapeptide motif -
XX
XX
PS Claim 16: Page 34, 47pp; English.

XX The invention relates to a ligand of less than 6 kD that binds to a
CC polypeptide containing the sequence GLYTYRGLYGLNPRHISGLYLY (A) or an
CC analogue that is the retro-inverso isomer of (A). The sequence A is
CC an octapeptide motif from the prion protein (PrP). The ligands are
CC identified by binding assays with the peptide (A) or peptides containing
CC (A). The ligands are used for detecting prion proteins (or prions) in
CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jakob diseases (in
CC latrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strausser-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is a ligand of the invention.

Sequence 6 AA:

Query Match 100.0%; Score 34; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6
1 |||||
DB 1 LTIWIP 6

RESULT 2

ABB40848
ID ABB40848 standard; Peptide: 87 AA.

XX ABB40848;

DT 04-FEB-2002 (first entry)

XX Peptide #8354 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

XX 09-AUG-2001.

PE 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -

PS Claim 27; SEQ ID NO 33483; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal

CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp:wipo.int/pub/published_pct_sequences.

Sequence 87 AA:

Query Match 100.0%; Score 34; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6
48 |||||
DB 48 LTIWIP 53

RESULT 3

ABB25012
ID ABB25012 standard; Protein: 87 AA.

XX ABB25012;

DT 23-JAN-2002 (first entry)

DE Protein #7011 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

XX 09-AUG-2001.

PE 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -

PS Claim 15; SEQ ID NO 26782; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see

CC ABA21535-ABA41305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying

CC gene expression in samples derived from the human heart via microarrays.

CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease.

CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp:wipo.int/pub/published_pct_sequences.

SQ Sequence 87 AA:

Query Match 100.0%; Score 34; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
Db 48 LLIWIP 53

RESULT 4
AAM61707
ID AAM61707 standard; Protein: 87 AA.

AC AAM61707;

DT 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 33812.

XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -

PS Example 4; SEQ ID NO: 33812; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention.

SQ Sequence 87 AA:

Query Match 100.0%; Score 34; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
Db 48 LLIWIP 53

RESULT 5
AAM74503

ID AAM74503 standard; Protein: 87 AA.

AC AAM74503;

DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 34809.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -

PS Example 4; SEQ ID NO: 34809; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention.

SQ Sequence 87 AA:

Query Match 100.0%; Score 34; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
Db 48 LLIWIP 53

RESULT 6
AAM34616
ID AAM34616 standard; Protein: 87 AA.

AC AAM34616;

DT 17-OCT-2001 (first entry)

XX Peptide #8653 encoded by probe for measuring placental gene expression.

XX Probe: microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.
 XX
 PF 30-JAN-2001. 2001MO-US00663.
 XX
 PR 04-FEB-2000. 2000US-0180312.
 PR 26-MAY-2000. 2000US-0207456.
 PR 30-JUN-2000. 2000US-0608408.
 PR 03-AUG-2000. 2000US-0632366.
 PR 21-SEP-2000. 2000US-0234687.
 PR 27-SEP-2000. 2000US-0236359.
 PR 04-OCT-2000. 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR.
 XX
 DR WPI; 2001-488997/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 analyzing gene expression in human placenta -
 Claim 27; SEQ ID NO 34885; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 XX
 SQ Sequence 87 AA:
 XX
 XX
 Query Match 100.0%; Score 34; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LLIWIP 6
 |||||
 Db 48 LLIWIP 53
 XX
 Db
 RESULT 7
 ID ABG44369
 ABG44369 standard; Peptide; 87 AA.
 XX
 AC ABG44369;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 Human peptide encoded by genome-derived single exon probe SEQ ID 34034.
 XX
 KM Human: single exon probe; asthma; lung cancer; COPD; ILD;
 KM chronic obstructive pulmonary disease; interstitial lung disease;
 KM familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KM tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KM Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KM pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KM pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KM primary ciliary dyskinesia; pulmonary hypertension;
 KM hyaline membrane disease.
 KM
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 XX 30-JAN-2001. 2001MO-US00665.
 PE
 PR 04-FEB-2000. 2000US-180312P.
 PR 26-MAY-2000. 2000US-207456P.
 PR 30-JUN-2000. 2000US-0608408.
 PR 03-AUG-2000. 2000US-0632366.
 PR 21-SEP-2000. 2000US-0234687.
 PR 27-SEP-2000. 2000US-0236359.
 PR 04-OCT-2000. 2000GB-0024263.

PR 21-SEP-2000. 2000US-234687P.
 PR 27-SEP-2000. 2000US-236359P.
 PR 04-OCT-2000. 2000GB-0024263.
 XX
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR.
 XX
 DR WPI; 2002-114183/15.
 XX
 DR
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 PS Claim 27; SEQ ID NO 34034; 634bp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridize at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 87 AA:
 XX
 XX
 Query Match 100.0%; Score 34; DB 23; Length 87;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LLIWIP 6
 |||||
 Db 48 LLIWIP 53
 XX
 Db
 RESULT 8
 AAB26446
 ID AAB26446 standard; Protein; 269 AA.
 XX
 AC AAB26446;
 XX

DT 23-FEB-2001 (first entry)
XX
PA Drosophila melanogaster odorant receptor DOR59.
DE
XX
XX Odorant receptor; fruit fly; DOR59; odour recognition; pest control.
XX
XX Drosophila melanogaster.
OS
PN WO200050566-A2.
XX
XX 31-AUG-2000.
PD
XX
XX 25-FEB-2000; 2000WO-US04995.
PF
XX
XX 25-FEB-1999; 99US-0257706.
PR
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
PA
XX
XX Vossball LB, Amrein HO, Axel R;
PI
XX WPI: 2000-572081/53.
XX N-PSDB; AAA94845.
PT Novel nucleic acid encoding an insect odorant receptor, for identifying
XX modulator compounds that are useful in controlling pest population
XX
XX
XX Disclosure; Page 75; 176pp; English.
PS
XX
XX The present sequence is the previously identified Drosophila melanogaster
CC odorant receptor DOR59. The odorant genes and proteins, such as those
CC provided by the invention, are useful as they aid in the study of the
CC olfactory organ in mammals, as well as aiding the understanding of the
CC link between odour recognition and behaviour in insects. They also enable
CC the identification of compounds capable of activating and inhibiting the
CC receptors, allow the control of pest populations via the use of alarm
CC odour ligands and via the use of ligands which interfere with the
CC interaction between odorant ligands and receptors associated with
CC fertility.
CC
XX
XX Sequence 269 AA:
SQ
Query Match 100.0%; Score 34; DB 21; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTIWIP 6
DB |||||
24 LTIWIP 29
RESULT 9
AAB68723
ID ABB68723 standard; Protein; 269 AA.
XX
XX ABB68723;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 32961.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PS

XX
XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI: 2001-656860/75.
DR
XX N-PSDB; ABL12826.
DR
XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
XX Disclosure; SEQ ID NO 32961; 21pp + Sequence Listing; English.
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL101840-ABL16175) and the encoded proteins
CC (AAB57737-AAB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
CC
XX
XX Sequence 269 AA:
SQ
Query Match 100.0%; Score 34; DB 22; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTIWIP 6
DB |||||
24 LTIWIP 29
RESULT 10
AAB20922
ID AAB20922 standard; Protein; 453 AA.
XX
XX AAB20922;
AC
XX
XX 06-DEC-2000 (first entry)
DT
XX
XX Drosophila odorant receptor DOR 56E.1.
DE
XX
XX Odorant receptor; Drosophila; olfactory receptor;
KW G protein-coupled receptor; GPCR superfamily; transgenic insect;
KW insect behaviour modification; pest control; pollinator attraction;
KW biosensor; odour detection; odour identification; apiculture.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200043410-A2.
PN
XX
XX 27-JUL-2000.
PD
XX
XX 25-JAN-2000; 2000WO-US01823.
PF
XX
XX 25-JAN-1999; 99US-0117132.
PR
XX
XX (UYVA) UNIV YALE.
PA
XX
XX Carlson JR, Kim J, Clyne PJ, Warr CG;
PI
XX
XX WPI: 2000-543246/49.
DR
XX N-PSDB; AAA72257.
DR
XX
XX New nucleic acid encoding a Drosophila olfactory receptor, useful for
PT identifying modulating agents -
XX
XX
XX Claim 12; Page 175-177; 303pp; English.
PS

XX Sequences AAB20901-B20949 represent *Drosophila melanogaster* odorant
CC receptors. These proteins function as olfactory receptors, and
CC are thought to be members of the G protein-coupled receptor
CC (GPCR) superfamily, which is characterised by the presence of 7
CC transmembrane helices. Nucleic acids encoding the *Drosophila* odorant
CC receptors may be used to generate expression constructs, host cells
CC containing such constructs, and transgenic insects. Cells which express
CC the odorant receptor genes may be used in methods to identify agents
CC which modulate expression of these genes, and in methods to identify
CC receptor binding partners. The *Drosophila* odorant receptor nucleic acids
CC may also be used to identify corresponding genes in other insects,
CC such as those which damage crops or transmit disease. The odorant
CC receptor proteins may be used to identify agents which modulate their
CC activity, to identify binding partners, as antigens to raise antibodies,
CC and in methods to modify insect behaviour. The proteins may be also
CC be used in methods of behaviour modification. Such methods may be used
CC to study or modify insect behaviour in response to odorants such as
CC pheromones. Modification of insect behaviour has a wide range of
CC applications, such as in pest control (e.g., by disrupting the feeding
CC or mating behaviours of pest species), or for enhancing plant
CC pollination (by attracting pollinator species). Odorant receptor proteins
CC and/or nucleotides may also be used to identify appetite suppressants, to
CC trap odours of a specific type, as biosensors for the detection of
CC explosives, drugs, perfumes or pollutants, and in apiculture to modify
CC the behaviour of bees, for example, to increase the production of royal
CC jelly.

SO Sequence 453 AA:

Query Match

Best Local Similarity 100.0%; Score 34; DB 21; Length 453;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6
| | | | |
DB 159 LTIWIP 164

RESULT 11

AAU14133

ID AAU14133 standard; Protein: 554 AA.

AC AAU14133;

DT 24-OCT-2001 (first entry)

XX Human novel protein #4.

Human: novel protein; Antianemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnary; nocrotic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antitubercular; dermatological; haemostatic; antiasmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.

OS Homo sapiens.

PN WO200155437-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02623.

PR 25-JAN-2000; 2000US-0491404.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-451939/48.

DR N-PSDB; JAS22438.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX Example 4; Page 522-523; 894pp; English.

XX The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.

SO Sequence 554 AA:

Query Match

Best Local Similarity 100.0%; Score 34; DB 22; Length 554;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6
| | | | |
DB 138 LTIWIP 143

RESULT 12

ABB92828

ID ABB92828 standard; Protein: 754 AA.

AC ABB92828;

DT 31-MAY-2002 (first entry)

XX Herbicidally active polypeptide SEQ ID NO 2039.

XX Herbicidal; plant; agriculture; herbicide.

XX Arabidopsis thaliana.

OS WO200210210-A2.

PN 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EF09892.

PR 28-AUG-2001; 2001WO-EF09892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

XX WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,
comprising aligning and comparing nucleic acid or amino acid sequences

PT from plant with nucleic acid or amino acid sequences from non-plant
XX organisms -
XX
PS Claim 5; SEQ ID NO 2039; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (AB90790-AB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 754 AA;
XX
Query Match 100.0%; Score 34; DB 23; Length 754;
PT Best Local Similarity 100.0%; Pred. No. 4.7e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 LTIWIP 6
XX |||||
DB 19 LTIWIP 24
XX
RESULT 13
AAAY24023
ID AAAY24023 standard; Protein; 298 AA.
XX
AC AAAY24023;
XX
DT 30-SEP-1999 (first entry)
XX
DE Human CMRF-35-H9 receptor protein.
XX
XX CMRF-35-H9 receptor; immunoglobulin M; IgM; immunomodulation;
XX humoral immune response; transplant; myeloid leukemia;
XX promyelocytic leukemia; leukemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 10
FT /note="encoded by CTC"
XX
PN WO9936438-A1.
XX
22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-NZ00003.
XX
PR 14-JAN-1998; 98NZ-0329582.
XX
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
XX
PI Hart DNF;
XX
XX WPI: 1999-458446/38.
XX DR N-PSDB; AAX86359.
XX
XX Human immunoglobulin M receptor CMRF-35-H9, useful for
PT immunomodulation
XX
XX Claim 3; Page 33; 40pp; English.
XX
XX The present sequence represents a novel receptor, CMRF-35-H9, which binds
CC immunoglobulin M (IgM). CMRF-35-H9, a CMRF-35-H9 extracellular domain
CC peptide or a vector encoding these, can be used to modulate an immune
CC response in a patient or to block or inhibit a humoral immune response
CC in a patient. This is particularly useful in a patient who has or is
CC about to receive a transplant. The CMRF-35-H9 receptor or extracellular
CC domain binds to antibodies, which are then no longer free to bind to the

CC transplant. A ligand/antigen construct that binds CMRF-35-H9 can be used
CC to load a protective antigen or a stimulatory antigen into an antigen
CC presenting cell. The level of CMRF-35-H9 in a patient sample can be
CC determined to diagnose myeloid leukemia in a patient. An increased level
CC of CMRF-35-H9 or decreased level of promyelocytic leukemia is diagnostic
CC of leukemia.
XX
SQ Sequence 298 AA;
XX
Query Match 97.1%; Score 33; DB 20; Length 298;
PT Best Local Similarity 83.3%; Pred. No. 2.8e+02;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX 1 LTIWIP 6
XX |||||
DB 8 LTIWIP 13
XX
RESULT 14
AAAY24022
ID AAAY24022 standard; Protein; 301 AA.
XX
AC AAAY24022;
XX
DT 30-SEP-1999 (first entry)
XX
DE Human CMRF-35-H9 receptor protein.
XX
XX CMRF-35-H9 receptor; immunoglobulin M; IgM; immunomodulation;
XX humoral immune response; transplant; myeloid leukemia;
XX promyelocytic leukemia; leukemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..13
FT /label= signal_peptide
FT Misc-difference 10
FT /note="encoded by CTC"
FT Protein 14..301
FT /label= mature_protein
FT Domain 29..126
FT /note="putative igm binding domain"
FT Region 178..201
FT /note="transmembrane region"
XX
PN WO9936438-A1.
XX
22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-NZ00003.
XX
PR 14-JAN-1998; 98NZ-0329582.
XX
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
XX
PI Hart DNF;
XX
XX WPI: 1999-458446/38.
XX DR N-PSDB; AAX86358.
XX
XX Human immunoglobulin M receptor CMRF-35-H9, useful for
PT immunomodulation
XX
XX Claim 12; Fig 2; 40pp; English.
XX
XX The present sequence represents a novel receptor, CMRF-35-H9, which binds
CC immunoglobulin M (IgM). CMRF-35-H9, a CMRF-35-H9 extracellular domain
CC peptide or a vector encoding these, can be used to modulate an immune
CC response in a patient or to block or inhibit a humoral immune response
CC in a patient. This is particularly useful in a patient who has or is
CC about to receive a transplant. The CMRF-35-H9 receptor or extracellular
CC domain binds to antibodies, which are then no longer free to bind to the

CC transplant. A ligand/antigen construct that binds CMRF-35-H9 can be used
 CC to load a protective antigen or a stimulatory antigen into an antigen
 CC presenting cell. The level of CMRF-35-H9 in a patient sample can be
 CC determined to diagnose myeloid leukemia in a patient. An increased level
 CC of CMRF-35-H9 or decreased level of promyelocytic leukemia is diagnostic
 CC of leukemia.

XX SQ Sequence 301 AA;

Query Match 97.1%; Score 33; DB 20; Length 301;

Best Local Similarity 83.3%; Pred. No. 2.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6

DB 8 LTIWIP 13

RESULT 15

AA53332 AAR53332 standard; Protein; 128 AA.

AC AAR53332;

DT 17-NOV-1994 (first entry)

DE KM-603 light chain.

XX Monoclonal antibody; Ab; ganglioside GM2; chimera;

KW chimeric antibody; expression vector; heavy; light; chain;

KM hypervariable region; CDR; constant region; hybridoma;

KW Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer.

XX Rat rattus.

OS Rat rattus.

EH Key Location/Qualifiers

FT Peptide 1..20

FT /label= sig_peptide

FT Region 44..54

FT /label= CDR1

FT Region 70..76

FT /label= CDR2

FT Region 109..117

FT /label= CDR3

XX AU9346181-A.

XX 17-MAR-1994.

XX 07-SEP-1993; 93AU-0046181.

XX 07-SEP-1992; 92JP-0238452.

XX (KYOW) KYOMA HAKKO KOGYO KK.

XX Hanai N, Hasegawa M, Kolke M, Kuwana Y, Nakamura X;

XX Shitara K;

XX MPI: 1994-126857/16.

XX N-PSDB; AAQ45430.

XX Humanised antibody specific for ganglioside GM2 - used for

XX producing a cytotoxic effect on cancers such as melanoma,

XX neuroblastoma and glioma.

XX Disclosure: Page 110; 191pp; English.

XX Chimeric human Ab expression vectors are constructed by inserting

XX the Ab heavy and light chain variable region-encoding CDNA

XX isolated from hybridomas producing a mouse or rat monoclonal Ab

XX reacting with the ganglioside GM2 respectively into an expression

XX vector for use in animal cells which contains the human Ab heavy and

XX light chain constant region-encoding CDNA. The expression vectors

XX

XX

XX

CC are introduced into animal cells and the transformant thus obtained
 CC is cultured for the prodn. of a chimeric human Ab reacting with the
 CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric
 CC human Abs will not cause anti-mouse Ig Ab prodn. in the patient's
 CC body but show a prolonged blood half-life, with a reduced frequency
 CC of adverse effects, so that it can be expected to be superior
 CC to mouse monoclonal Abs in the efficacy in the treatment of human
 CC cancer, for instance.

XX SQ Sequence 128 AA;

Query Match 94.1%; Score 32; DB 15; Length 128;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6

DB 11 LTIWIP 16

Search completed: January 3, 2003, 15:28:35
 Job time : 27.5909 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:00 ; Search time 9.95455 Seconds
(without alignments)
57.944 Million cell updates/sec

Title: US-09-543-188A-3

Perfect score: 34

Sequence: 1 LLIWIP 6

Scoring table: BLASTUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues
al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	367	2 F70036	capsular polysach
2	34	100.0	402	2 S65973	transport protein
3	34	100.0	554	2 S71751	dolichyl-phosphate
4	34	100.0	754	2 A85043	probable LRR recep
5	34	100.0	2452	1 RN202L	DNA-directed RNA p
6	34	100.0	2457	2 T18492	hypothetical prote
7	33	97.1	171	2 CA5665	adult-specific bru
8	33	97.1	304	2 S69034	probable membrane
9	32	94.1	126	2 S40312	Ig kappa chain - h
10	32	94.1	200	2 G83834	hypothetical prote
11	32	94.1	269	2 T15500	hypothetical prote
12	32	94.1	501	2 G82822	NADH2 dehydrogenas
13	32	94.1	542	2 T19862	hypothetical prote
14	31	91.2	114	2 S00996	Ig kappa chain pre
15	31	91.2	115	2 S10146	Ig kappa chain pre
16	31	91.2	117	2 S24207	Ig kappa chain V r
17	31	91.2	120	2 S06731	Ig kappa chain pre
18	31	91.2	120	2 S06732	Ig kappa chain pre
19	31	91.2	128	2 J10073	aberrant kappa tra
20	31	91.2	131	1 KWSM6	Ig kappa chain pre
21	31	91.2	131	2 PH1226	Ig kappa chain pre
22	31	91.2	131	2 S55027	Ig light chain pre
23	31	91.2	132	2 G83872	hypothetical prote
24	31	91.2	131	1 KWSM32	Ig kappa chain pre
25	31	91.2	140	2 PNO446	Ig kappa chain pre
26	31	91.2	157	2 B86424	unknown protein, 3
27	31	91.2	229	2 T34215	Fc gamma (IgG) rec
28	31	91.2	280	2 S55577	Fc gamma (IgG) rec
29	31	91.2	336	2 I48471	Fc gamma (IgG) rec

30	31	91.2	344	2 A41357	Fc gamma (IgG) rec
31	31	91.2	349	2 B86603	muramoyl-pentapept
32	31	91.2	349	2 G72021	muramoyl-pentapept
33	31	91.2	349	2 A81519	phospho-N-acetylmu
34	31	91.2	365	2 A48105	probable M-factor
35	31	91.2	374	1 A39878	Fc gamma (IgG) rec
36	31	91.2	396	1 B65169	multidrug resistanc
37	31	91.2	396	2 F91205	2-module integral
38	31	91.2	396	2 H86051	2-module integral
39	31	91.2	404	2 A46480	Fc gamma (IgG) rec
40	31	91.2	431	2 H84069	hypothetical prote
41	31	91.2	443	2 C71904	anaerobic c4-dicar
42	31	91.2	443	2 D64610	dicarboxylate memb
43	31	91.2	500	2 AF2325	NADH dehydrogenase
44	31	91.2	512	2 T15669	hypothetical prote
45	31	91.2	741	2 A83271	hypothetical prote

ALIGNMENTS

RESULT 1
F70036
capsular polysaccharide biosynthesis homolog yveQ - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: F70036
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funna, S.; Gallizzi, A.; Gal
isch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F70036
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-367 <KUN>
A:Cross-references: GB:299121; GB:AL009126; NID:92635827; PIDN:CAB15436.1; PID:el1861
A:Experimental source: strain 168
C:Genetics:
A:Gene: yveQ
Query Match 100.0%; Score 34; DB 2; Length 367;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLIWIP 6
Db 37 LLIWIP 42
RESULT 2
S65973
transport protein homolog yycB - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S65973; A70089
R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.
A:Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis ch
A:Reference number: S65967; MUID:96051385; PMID:7584024
A:Accession: S65973
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-2457 <LAW>
A:Cross-references: EMBL:Z98551; PIDN:CAB1131.1
C:Genetics:
A:Map position: 3
A>Note: C0805W
C:Superfamily: Plasmodium DNA-directed RNA polymerase II large chain

Query Match 100.0%; Score 34; DB 2; Length 2457;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
|||||
DB 582 LLIWIP 587

RESULT 7

■ It-specific brush border protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C:Accession: C45665
R:Boil, W.; Schmid-Chanda, T.; Semenza, G.; Mantel, N.
J. Biol. Chem. 268, 12901-12911, 1993
A:Title: Messenger RNAs expressed in intestine of adult but not baby rabbits. Isolation

A:Reference number: A45665; MUID:93286138; PMID:8509424

A:Accession: C45665

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-171 <BO>

A:Cross-references: GB:Z12842; NID:q1763; PIDN:CA78304.1; PID:q1764
C:Superfamily: rabbit adult-specific brush border protein

C:Keywords: intestine; transmembrane protein

Query Match 97.1%; Score 33; DB 2; Length 171;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
|||||
DB 63 LLIWIP 68

RESULT 8

S69034

■ Double membrane protein YPR147c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002

C:Accession: S69034

R:Fulton, L.

Submitted to the EMBL Data Library, November 1995

A:Description: The sequence of S. cerevisiae cosmid 9659.

A:Reference number: S69022

A:Accession: S69034

A:Molecule type: DNA

A:Residues: 1-304 <FU>

A:Cross-references: EMBL:U40829; NID:q1066476; PID:q1066494; GSPDB:GN00016; MIPS:YPR147C

C:Genetics:

A:Gene: MIPS:YPR147C

A:Cross-references: SGD:S0006351

A:Map position: 16R

C:Keywords: transmembrane protein

Query Match 97.1%; Score 33; DB 2; Length 304;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
|||||
DB 31 LLIWIP 36

RESULT 9

S40312

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40312

R:Klein, R.; Jernichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40312

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-126 <KLE>

A:Cross-references: EMBL:X72422; NID:q441312; PID:q441313

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 94.1%; Score 32; DB 2; Length 126;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
|||||
DB 4 LLIWIP 9

RESULT 10

G83834

hypothetical protein BH1479 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: G83834

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a

A:Reference number: A83650; MUID:20512582; PMID:11058152

A:Accession: G83834

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-200 <STO>

A:Cross-references: GB:AP001512; GB:BA000004; NID:q10174030; PIDN:BA05198.1; GSPDB:G

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH1479

Query Match 94.1%; Score 32; DB 2; Length 200;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
|||||
DB 193 LLIWIP 198

RESULT 11

T15500

hypothetical protein C15B12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000

C:Accession: T15500

R:Nhan, M.

Submitted to the EMBL Data Library, March 1995

A:Description: The sequence of C. elegans cosmid C15B12.

A:Reference number: Z18362

A:Accession: T15500

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-269 <NHA>

A:Cross-references: EMBL:U23529; NID:q746592; PID:q746594; PIDN:AAC46577.1; CESP:C15B

A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C15B12.2
A:Introns: 3/3; 49/3; 105/2; 200/2; 245/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C15B12.2

Query Match
Best Local Similarity 94.1%; Score 32; DB 2; Length 269;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
||||:|
Db 76 LLIWIP 81

RESULT 12

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Xylella fastidiosa
C:Species: Xylella-fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Jun-2002
Accession: G82822

Annotation: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82822

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-501 <SIM>

A:Cross-references: GB:AE00384; GB:AE003849; NID:g9105127; PIDN:AAF83128.1; GSPDB:GN001

A:Experimental source: strain 965c

R:Simposon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
B:Simposon, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carro, D.M.; Carre, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincanl, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurama, E.E.; Laigt
chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeiri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0317

Superfamily: NADH dehydrogenase (ubiquinone) chain 4

Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match
Best Local Similarity 94.1%; Score 32; DB 2; Length 501;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
||||:|
Db 9 LLIWIP 14

RESULT 13

hypothetical protein C40C9.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19862

R:Hemby, C.

submitted to the EMBL Data Library, March 1996

A:Accession: T19862

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-542 <MIL>

A:Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2

A:Experimental source: clone C40C9

C:Genetics:

A:Gene: CESP:C40C9.2

A:Map position: X

A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;

C:Superfamily: acetylcholine receptor

Query Match
Best Local Similarity 94.1%; Score 32; DB 2; Length 542;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
||||:|
Db 355 LLIWIP 360

RESULT 14

S00996
Ig kappa chain precursor V region (A10) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999

C:Accession: S00996

R:Strubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.

Biol. Chem. Hoppe-Seyler 369, 601-607, 1988

A:Title: Two unusual human immunoglobulin V-kappa genes.

A:Reference number: S00996; MUID:89134397; PMID:2852016

A:Accession: S00996

A:Molecule type: DNA

A:Residues: 1-114 <STR>

A:Cross-references: EMBL:M27750; NID:q185914; PIDN:AAAS8912.1; PID:g553479

A:Note: this sequence was determined from the germline gene

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-114/Product: Ig kappa chain V region #status predicted <MAT>

F:42-107/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 91.2%; Score 31; DB 2; Length 114;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
||||:|
Db 10 LLIWIP 15

RESULT 15

S10146
Ig kappa chain precursor V region (A14) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000

C:Accession: S10146

R:Strubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.

Biol. Chem. Hoppe-Seyler 369, 601-607, 1988

A:Title: Two unusual human immunoglobulin V-kappa genes.

A:Reference number: S00996; MUID:89134397; PMID:2852016

A:Accession: S10146

A:Molecule type: DNA

A:Residues: 1-115 <STR>

A:Cross-references: EMBL:M27751; NID:q185916; PIDN:AAAS8913.1; PID:g185917

A:Note: this sequence was determined from the germline gene

C:Genetics:

A:Introns: 17/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V region #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

F:43-108/Disulfide bonds: #status predicted

Mon Jan, 6 15:09:02 2003

us-09-543-188a-3.rpr

Page 5

Query Match 91.2%; Score 31; DB 2; Length 115;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
Db 11 LLIWIP 16

Search completed: January 3, 2003, 15:33.15
Job time : 11.9545 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:22:10 : Search time 5.18182 Seconds
(without alignments)
48.025 Million cell updates/sec

Title: US-09-543-188A-3
Perfect score: 34
Sequence: 1 LLWIP 6

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	402	1 YTCB_BACSU	P37482 bacillus su
2	34	100.0	419	1 O56A_DROME	Q948Y7 drosophila
3	34	100.0	2452	1 RPBI_PLARD	P14248 plasmodium
4	33	97.1	171	1 BB19_RABIT	O05005 oryctolagus
5	31	91.2	131	1 KV3I_MOUSE	P01651 mus musculu
6	31	91.2	132	1 KV3F_MOUSE	P01658 mus musculu
7	31	91.2	335	1 MFI1_KLJDA	P87250 kluyveromyc
8	31	91.2	349	1 MRAY_CHLPP	Q94706 chlamydia p
9	31	91.2	365	1 MAP3_SCHPO	P31397 schizosacch
10	31	91.2	374	1 FCGI_HUMAN	P12314 homo sapien
11	31	91.2	394	1 EMDR_ECOLI	P31442 escherichia
12	31	91.2	404	1 FCGI_MOUSE	P26151 mus musculu
13	31	91.2	443	1 DCVA_HELPY	Q921C0 helicobacte
14	31	91.2	443	1 DCVA_HELPY	O25425 helicobacte
15	30	88.2	115	1 KV3I_HUMAN	P04433 homo sapien
16	30	88.2	115	1 KV3I_MOUSE	P01642 mus musculu
17	30	88.2	116	1 KV3I_HUMAN	P04434 homo sapien
18	30	88.2	117	1 KV3I_HUMAN	P01602 homo sapien
19	30	88.2	117	1 YCCI_YEAST	P23561 saccharomyc
20	30	88.2	128	1 KV3K_HUMAN	P04207 homo sapien
21	30	88.2	129	1 KV3H_HUMAN	P04207 homo sapien
22	30	88.2	129	1 KV3I_HUMAN	P18135 homo sapien
23	30	88.2	129	1 KV3M_HUMAN	P18136 homo sapien
24	30	88.2	164	1 Y40B_HRISN	P53623 rhizobium s
25	30	88.2	240	1 P4SC_HAEIN	P44848 haemophilus
26	30	88.2	310	1 YGRI_YEAST	P53108 saccharomyc
27	30	88.2	319	1 NUIM_POLOR	O96182 polypierus
28	30	88.2	337	1 MPFL_SACKL	P87292 saccharomyc
29	30	88.2	348	1 Y567_HELPY	O25291 helicobacte
30	30	88.2	349	1 Y567_HELPY	O25291 helicobacte
31	30	88.2	392	1 CEWA_NEPOL	O91KZ2 neptosein
32	30	88.2	467	1 GAC3_HUMAN	O99928 homo sapien
33	30	88.2	467	1 GAC3_MOUSE	P27681 mus musculu

34	30	88.2	467	1 GAC3_RAT	P28473 rattus norv
35	30	88.2	503	1 ALG6_CAEEL	O09226 caenorhabd
36	30	88.2	575	1 ITR1_SCHPO	O10786 schizosacch
37	30	88.2	631	1 YC10_ECOLI	P45848 escherichia
38	30	88.2	710	1 IGAA_SALTY	P58721 salmoneila
39	30	88.2	710	1 IGAA_SALTY	O94CPO salmoneila
40	30	88.2	711	1 IGAA_ECO57	P58720 escherichia
41	30	88.2	711	1 IGAA_ECOLI	P45800 escherichia
42	30	88.2	1541	1 MRP2_RAT	O63120 rattus norv
43	30	88.2	1545	1 MRP2_HUMAN	O92887 homo sapien
44	30	88.2	1564	1 MRP2_RABIT	Q28689 oryctolagus
45	29	85.3	115	1 MYHA_MOUSE	O61879 mus musculu

ALIGNMENTS

RESULT 1
ID YTCB_BACSU STANDARD: PRT: 402 AA.
AC P37482;
DT 01-OCT-1994 (rel. 30, Created)
DT 01-OCT-1994 (rel. 30, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Hypothetical transport protein ytcB.
GN YTCB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capano V., Carter N.M.,
Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
Dentzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Fougere D.,
Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,
Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klier-Blandhard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapdus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel J., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetlelle D., Porwollik S., Prescott A.M.,
Preescan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Roche E., Roche B., Rose M., Satale Y.,
Sato T., Scanlan E., Schleich S., Schroeder R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Yamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassaretti A.,
Viari A., Mamput R., Medler E., Medler H., Weitzenecker T.,
Winners P., Wipat A., Yamamoto H., Yamane K., Yasuno K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumsstein E., Yoshikawa H., Darchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).

CC -1- SIMILARITY: BELONGS TO THE TC 2.A.1.17.1 TRANSPORTER FAMILY.

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CC EMBL: D26185; BAA05179.1; -
CC EMBL: Z99124; CAB16085.1; -
CC Subtilisin; Bgi0007; yycb.
CC InterPro: IPR004747; Cyan_transport.
CC TIGRfam: TIGR00896; CynX; 1.
CC Hypothetical protein; Transport: Transmembrane; Complete proteome.
CC TRANSMEM 12 32
CC TRANSMEM 48 68 POTENTIAL.
CC TRANSMEM 80 100 POTENTIAL.
CC TRANSMEM 101 121 POTENTIAL.
CC TRANSMEM 134 154 POTENTIAL.
CC TRANSMEM 168 188 POTENTIAL.
CC TRANSMEM 212 232 POTENTIAL.
CC TRANSMEM 248 268 POTENTIAL.
CC TRANSMEM 291 311 POTENTIAL.
CC TRANSMEM 339 359 POTENTIAL.
CC TRANSMEM 367 387 POTENTIAL.
CC SO SEQUENCE 402 AA; 43184 MW; 45C3348FE2183CD CRC64;

Query Match 100.0%; Score 34; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTIWIP 6
| | | | |
DB 181 LTIWIP 186

RESULT 2
056A_DROME STANDARD; PRT: 419 AA.
AC Q9V877;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Putative odorant receptor 56a.
GN OR56A OR CG12501.
CC Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
CC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu L.B., Davies P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dubin K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,
RA Foster C., Garfield A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster.";
RA Science 287:2185-2195(2000).
[2]
RP REVISIONS.
RC STRAIN-Berkeley;
RC Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Cealinker S.E.,
RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
RA Harris N.L., Krommler B., Marshall B., Milburn G.H., Richter J.,
RA Russo S., Seale S.M.J., Smith E., Shu S., Smutnick F.,
RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Mungall C.J., Lewis S.E.;
RA "Annotation of Drosophila melanogaster genome.";
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
CC RECEPTORS.

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CC EMBL: AE003794; AAF57517.2; -
CC Flybase: FBgn0034473; Or56a.
CC InterPro: IPR004117; 7tm_6.
CC Pfam: PF02949; 7tm_6; 1.
CC Hypothetical protein; Transmembrane; G-protein coupled receptor;
CC Olfaction; Multigene family.
CC TRANSMEM 1 41
CC TRANSMEM 42 62 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 63 76 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 77 97 2 (POTENTIAL).
CC TRANSMEM 98 137 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 138 158 3 (POTENTIAL).
CC TRANSMEM 159 196 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 197 217 4 (POTENTIAL).
CC TRANSMEM 218 292 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 293 313 5 (POTENTIAL).
CC TRANSMEM 314 323 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 324 344 6 (POTENTIAL).
CC TRANSMEM 345 389 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 390 410 7 (POTENTIAL).
CC TRANSMEM 411 419 CYTOPLASMIC (POTENTIAL).
CC SO SEQUENCE 419 AA; 48920 MW; F5F8254502560040 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 419;
Best Local Similarity 100.0%; Pred. No. 27;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LTIWIP 6
 |||||
 Db 140 LTIWIP 145

RESULT 3
 REP1_PLAFD
 ID REP1_PLAFD STANDARD; PRT: 2452 AA.

AC P14248;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6).
 GN RPII.
 OS Plasmodium falciparum (isolate CDC / Honduras).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5836;
 [1]

SEQUENCE FROM N.A.

MEDLINE-90098932; PubMed-2690004;
 RA Li W.B., Beik D.J., Gu H., Tanaka M., Fox B.A., Inselburg J.;
 RT "An enlarged largest subunit of Plasmodium falciparum RNA polymerase
 II defines conserved and variable RNA polymerase domains.";
 RL Nucleic Acids Res. 17:9621-9636(1989).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 (RNA)(N).
 CC -1- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM TEN TO
 TWELVE DIFFERENT POLYPEPTIDES. THIS POLYPEPTIDE IS THE LARGEST
 COMPONENT OF RNA POLYMERASE II.

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- PTM: THE TANDAM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
 CC THE PHOSPHORYLATION ACTIVATES POL2.

CC -1- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WERE
 FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
 PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
 III FOR 5S AND TRNA GENES.

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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CC EMBL: X16561; CAA34560.1; -
 DR PIR: S07485; RNZ02L.
 DR InterPro: IPR000684; RNA_polII_repeat.
 DR InterPro: IPR000722; RNA_pol_A.
 DR InterPro: IPR002879; RNA_pol_A2.
 DR Pfam: PF00623; RNA_pol_A; 1.
 DR Pfam: PF01854; RNA_pol_A2; 1.
 DR PROSITE: PS00115; RNA_POL_II_REPEAT; 9.
 DR Transfaser: DNA-directed RNA polymerase; Transcription; Zinc; Repeat;
 KW DNA-binding; Nuclear protein; C2H2-type (POTENTIAL); Zinc-finger.
 FT ZN_FING 68 84
 FT ZN_FING 378 411
 FT DNA_BIND 707 725
 FT DOMAIN 1093 1128
 FT DOMAIN 1144 1159
 FT DNA_BIND 1182 1193
 FT DOMAIN 1687 1694
 FT DOMAIN 1258 1290
 FT DOMAIN 1261 1290
 FT DOMAIN 1602 1612
 FT DOMAIN 1746 1759
 FT DOMAIN 1806 1820

FT DOMAIN 2061 2246 HIGHLY DIVERGED HEPTAPEPTIDE REPEATS.
 FT DOMAIN 2247 2384 CARBOXYL-TERMINAL 7-RESIDUE REPEATS.
 SQ SEQUENCE 2452 AA; 278166 MW; F995E117F617A48F CRC64;

Query Match
 Best Local Similarity 100.0%; Score 34; DB 1; Length 2452;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTIWIP 6
 |||||
 Db 582 LTIWIP 587

RESULT 4
 BB19_RABIT
 ID BB19_RABIT STANDARD; PRT: 171 AA.

AC Q05005;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Brush border 19.3 kDa protein precursor.
 GN ADRAB-C.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-93286138; PubMed-8509424;
 RA Boll W., Schmid-Chanda T., Semenza G., Mantel N.;
 RT "Messenger RNAs expressed in intestine of adult but not baby rabbits.
 RT Isolation of cognate cDNAs and characterization of a novel brush
 border protein with esterase and phospholipase activity.";
 RL J. Biol. Chem. 268:12901-12911(1993).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: INTESTINE.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE INTESTINE OF ADULT BUT NOT
 BABY RABBITS.

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CC EMBL: Z12842; CAA78304.1; -
 DR PIR: C45665; C45665.
 DR Signal; Transmembrane.
 FT SIGNAL 1 21
 FT CHAIN 22 171
 FT TRANSMEM 49 69
 FT TRANSMEM 88 108
 FT TRANSMEM 131 151
 FT SEQUENCE 171 AA; 19290 MW; 1628238A011F9ADB CRC64;

Query Match
 Best Local Similarity 97.1%; Score 33; DB 1; Length 171;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTIWIP 6
 |||||
 Db 63 LTIWIP 68

RESULT 5
 KV31_MOUSE
 ID KV31_MOUSE STANDARD; PRT: 131 AA.

AC P01661;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region MOPC 63 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=78235887; PubMed=98179;
 RA Burslein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 RT the variable and constant regions of immunoglobulin light chain
 RT precursors: implications on the organization and controlled
 RT expression of immunoglobulin genes.";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-131.
 RX MEDLINE=73140225; PubMed=4691517;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 RT kappa chains with limited sequence differences.";
 RL Biochemistry 12:760-771(1973).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 DR HSP; P01679; 2FBU.
 DR HSP; P01679; KYMS6.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV: 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 59 73 FRAMEWORK-2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 81 112 FRAMEWORK-3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 131 FRAMEWORK-4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON_TER 131 131
 SO SEQUENCE 131 AA; 14291 MW; D212EC9F08DC860A CRC64;
 Query Match 91.2%; Score 31; DB 1; Length 131;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RT "Primary structures of N-terminal extra peptide segments linked to
 RT the variable and constant regions of immunoglobulin light chain
 RT precursors: implications on the organization and controlled
 RT expression of immunoglobulin genes.";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-132.
 RX MEDLINE=73140224; PubMed=4120629;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
 RT chain.";
 RL Biochemistry 12:749-759(1973).
 CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
 CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
 CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
 CC RESIDUES.
 DR PIR; A01933; KYMS32.
 DR HSP; P01679; 2FBU.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_V.
 DR SMART: SM00406; IGV: 1.
 DR Immunoglobulin V region; Bence-Jones protein; signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 59 73 FRAMEWORK-2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 81 112 FRAMEWORK-3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 131 FRAMEWORK-4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON_TER 132 132
 SO SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FEB9 CRC64;
 Query Match 91.2%; Score 31; DB 1; Length 132;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
 DB 11 LLLWVP 16

RESULT 7
 ID MTF1_KL0LA STANDARD; PRT; 335 AA.
 AC P87250;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Mitochondrial replication protein MTF1 (Mitochondrial transcription
 DE factor MTFB).
 GN MTF1.
 OS Kluyveromyces fragilis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_TaxID=28965;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97339478; PubMed=9196077;
 RA Carodenas J.A., Yun S., Shadel G.S., Clayton D.A., Bogenhagen D.F.;
 RT "Functional conservation of yeast mtrfb despite extensive sequence
 RT divergence.";
 RL Gene Expr. 6:219-230(1996).
 CC -1- FUNCTION: ESSENTIAL FOR MITOCHONDRIAL REPLICATION AND
 CC TRANSCRIPTION. CONFERS SELECTIVE PROMOTER RECOGNITION ON THE CORE
 CC SUBUNIT OF THE YEAST MITOCHONDRIAL RNA POLYMERASE. INTERACTS WITH
 CC DNA IN A NON-SPECIFIC MANNER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- SIMILARITY: FAINT SIMILARITY WITH THE T4 GENE 32 PRODUCT AND WITH
 CC BACTERIAL SIGMA FACTORS.

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CC -----
DR EMBL: U81620; AAC49739.1; -
KW Mitochondrion; DNA replication; Transcription regulation; DNA-binding.
SQ SEQUENCE 335 AA; 39201 MW; 1E5EC6D7C6C3B791 CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 1; Length 335;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
   11111
   171 MLWIP 176

RESULT 8
MRAY_CHLPN STANDARD; PRT; 349 AA.
AC Q92706; Q9JS12;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-
DE MurNAC-pentapeptide phosphotransferase).
GN MRAY OR CPN0900 OR CP0966.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalan S., Mitchell W., Marathe R., Iamuel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., Debroy R., Koloney J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=1138;
RX MEDLINE=20330349; PubMed=10671362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayes J., Baker S., Basham S., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

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CC -----
DR EMBL: AE001670; AAD19038.1; -
DR EMBL: AE002254; AAF38746.1; -
DR EMBL: AP002548; BAA99108.1; -
DR TIGR: CP0966; -
DR InterPro: IPR000715; Glycos.transf.4.
DR InterPro: IPR003524; PNAcCP_transf.
DR Pfam: PF00953; Glycos.transf_4; 1.
DR TIGRPFAMs: TIGR00445; mray; 1.
DR PROSITE: PS01347; MRAY_1; 1.
DR PROSITE: PS01348; MRAY_2; 1.
KW Peptidoglycan synthesis; Cell division; Transferase; Transmembrane;
KW Complete proteome.
FT TRANSMEM 13 POTENTIAL.
FT TRANSMEM 69 POTENTIAL.
FT TRANSMEM 91 POTENTIAL.
FT TRANSMEM 129 POTENTIAL.
FT TRANSMEM 165 POTENTIAL.
FT TRANSMEM 197 POTENTIAL.
FT TRANSMEM 228 POTENTIAL.
FT TRANSMEM 252 POTENTIAL.
FT TRANSMEM 278 POTENTIAL.
FT TRANSMEM 327 POTENTIAL.
FT TRANSMEM 347 POTENTIAL.
FT TRANSMEM 370 POTENTIAL.
FT TRANSMEM 3859 MW; 60AA9283C594A8B CRC64;
SQ SEQUENCE 349 AA; 38589 MW; 60AA9283C594A8B CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 1; Length 349;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
   11111
   82 LVLWLP 87

RESULT 9
MAP3_SCHPO STANDARD; PRT; 365 AA.
AC P31397;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pheromone M-factor receptor.
GN MAP3 OR SPAC3F10.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ST711;
RX MEDLINE=93109361; PubMed=8380233;
RA Tanaka K., Davey J., Imai Y., Yamamoto M.;
RT "Schizosaccharomycetes pombe map3 encodes the putative M-factor
RT receptor.";
RL Mol. Cell. Biol. 13:80-88(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayes J., Baker S., Basham S., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

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RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckie E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Mblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quill M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkhardt G., Aert R., Robben J., Grymoprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moesli D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Ray F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovskii G.V., Usseery D., Barrell B.G., Nurse P.,
 RA "The genome sequence of Schizosaccharomyces pombe." ;
 RL Nature 415:871-880(2002).
 CC -I- FUNCTION: RECEPTOR FOR THE PEPTIDE PHEROMONE M-FACTOR, A MATING
 CC FACTOR OF S. POME. PHEROMONE SIGNALING IS ESSENTIAL FOR INITIATION
 CC OF MEIOSIS IN S. POME. M-FACTOR SIGNALING ALONE MAY BE SUFFICIENT.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- INDUCTION: BY AT LEAST 3 TYPES OF REGULATION: THE MATING-TYPE OF
 CC THE CELL, NUTRITIONAL CONDITIONS AND PHEROMONE SIGNALING.
 CC -I- SIMILARITY: BELONGS TO FAMILY 4 OF G-PROTEIN COUPLED RECEPTORS.

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 CC EMBL: D10933; BA01727.1; -;
 DR EMBL: Z69369; CA93308.1; -;
 DR PIR: A48105; A48105.
 DR InterPro: IPR001459; SRE3_GPCR.
 DR Pfam: PF02076; SRE3_1.
 KW Transmembrane; G-protein coupled receptor; Pheromone response.
 FT TRANSMEM 7 24 POTENTIAL.
 FT TRANSMEM 31 54 POTENTIAL.
 FT TRANSMEM 73 100 POTENTIAL.
 FT TRANSMEM 116 133 POTENTIAL.
 FT TRANSMEM 155 182 POTENTIAL.
 FT TRANSMEM 204 226 POTENTIAL.
 FT TRANSMEM 265 283 POTENTIAL.
 FT SEQUENCE 365 AA; 42498 MW; 306A022FA7DCFEF7 CRC64;

 QY Query Match 91.2%; Score 31; DB 1; Length 365;
 Db Best Local Similarity 66.7%; Pred. No. 85;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLIWIP 6
 ||:|:|
 Db 294 LLVWLP 299

 RESULT 10
 FCGL_HUMAN
 ID FCGL_HUMAN STANDARD; PRT; 374 AA.
 AC P12314; P12315;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE High affinity immunoglobulin gamma fc receptor I precursor (Fc-gamma
 RI) (FCRI) (IlgG Fc receptor 1) (CD64).
 GN FCGR1A OR FCGR1 OR FCGL OR IGRI.

[illegible]

FT VARSPLIC 333 374 HEKRVTSIQEDRHLEELKCOEQKEQLOEGVHRKEPOGA
FT T -> GOLEAPTOGCA (IN ISOFORM B).
FT VARIANT 26 26 L -> T
FT VARIANT 59 59 /FTid=VAR_003953.
FT VARIANT 59 59 N -> V.
FT CONFLICT 25 25 /FTid=VAR_003954.
FT SEQUENCE 374 AA: 42605 MW: 2C2AAB103ECF16E6 CRC64: S -> T (IN REF. 1: CAA32536).
SQ
Query Match 91.2%; Score 31; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLIWIP 6
DB 7 LLIWIP 12
RESULT 11
D_ECOLI
AC P31442; STANDARD: PRT; 394 AA.
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multidrug resistance protein D.
GN EMDR OR B3673.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RA MEDLINE=94059107; PubMed=8240555;
RA Narditskaya V., Schloesser M.J., Fan N.Y., Lewis R.;
RL "An E. coli gene emdr is involved in adaptation to low energy shock.";
RL Biochem. Biophys. Res. Commun. 196:803-809(1993).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93315143; PubMed=7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
genome: organizational symmetry around the origin of replication.";
RL Genomics 16:551-561(1993).
CC -1- FUNCTION: MULTIDRUG RESISTANCE PUMP THAT PARTICIPATES IN A LOW
ENERGY SHOCK ADAPTATIVE RESPONSE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(potential).
CC -1- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE
BCP/CMLA SUBFAMILY.
CC
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CC
CC EMBL: L10328; AAA62025.1; ALT_INIT.
DR EMBL: AE000445; AAC76696.1; ALT_INIT.
DR Ecogene: EG11693; emrd.
DR InterPro: IPR004734; Drug_resist.
DR InterPro: IPR003652; Sub_transp.
DR Pfam: PF00083; sugat.tr.1.
DR TIGRPFAMs: TIGR00880; 2.A_01_02: 1.
KW Transport; Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 9 29
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 96 116 POTENTIAL.

FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 277 297 POTENTIAL.
FT TRANSMEM 299 319 POTENTIAL.
FT TRANSMEM 330 350 POTENTIAL.
FT TRANSMEM 365 385 POTENTIAL.
SQ
Query Match 91.2%; Score 31; DB 1; Length 394;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLIWIP 6
DB 286 LLIWIP 291
RESULT 12
FCGL_MOUSE
ID FCGL_MOUSE STANDARD: PRT; 404 AA.
AC P26151;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE High affinity Immunoglobulin gamma FC receptor I precursor (FC-gamma
RI) (FCRI) (IGG FC receptor I).
GN FCGR1 OR FCGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RA MEDLINE=90111035; PubMed=2136886;
RX Sears D.W., Osman N., Tate B., McKenzie I.F.C., Hogarth P.M.;
RT "Molecular cloning and expression of the mouse high affinity FC
receptor for IgG.";
RL J. Immunol. 144:371-378(1990).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=92166399; PubMed=1531670;
RA Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;
RT "Structure and mapping of the gene encoding mouse high affinity FC
gamma RI and chromosomal location of the human FC gamma RI gene.";
RL J. Immunol. 148:1570-1575(1992).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS GAMMA. HIGH
AFFINITY RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: MACROPHAGE-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
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CC
CC EMBL: M31314; AAA40056.1; -
DR EMBL: PIR: A43511; A43511.
DR PIR: A46480; A46480.
DR HSSP: P12319; IALS.
DR MGP: MGI:95498; FCgr1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_like; 2.

DR SMART; SM00408; IGC2; 1.
 KW IGC-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KM Immunoglobulin domain; Repeat.
 FT SIGNAL 1 24
 FT CHAIN 25 404
 FT DOMAIN 25 297
 FT TRANSMEM 298 320
 FT DOMAIN 321 404
 FT DOMAIN 46 102
 FT DOMAIN 127 184
 FT DOMAIN 214 276
 FT DISULFID 53 95
 FT DISULFID 134 177
 FT DISULFID 221 269
 FT CARBOHYD 28 28
 FT CARBOHYD 48 48
 FT CARBOHYD 69 69
 FT CARBOHYD 168 168
 FT CARBOHYD 249 249
 SEQUENCE 404 AA: 44887 MW: 1CAFD03842767E7 CRC64:
 Query Match
 Best Local Similarity 91.2%; Score 31; DB 1; Length 404;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHWIP 6
 DB 16 LHWIP 21

RESULT 13

DCUA_HELPJ STANDARD: PRT: 443 AA.
 AC 09ZLC0:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Anaerobic C4-dicarboxylate transporter dcua.
 OS DCUA OR JHP0660.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.R., Ling L.-S.L., Molt D.T., King B.L., Brown E.D., Dotig P.C.,
 Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 Gibson R., Merberg D., Mills S.D., Jlang Q., Taylor D.E., Vovis G.F.,
 Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 gastric pathogen Helicobacter pylori."
 RL Nature 397:176-180(1999).
 CC -1- FUNCTION: RESPONSIBLE FOR THE TRANSPORT OF C4-DICARBOXYLATES FROM
 CC THE PERIPLASM ACROSS THE INNER MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein, inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE DCUA / DCUB (TC 2.A.13.1) FAMILY OF
 CC TRANSPORTERS.

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 CC -----
 CC EMBL: AE001498; AAD06239.1; -
 CC InterPro: IPR004668; Dcu.
 CC Pfam: PF03605; Dcu; 1.
 CC Trifams: TIGR00770; Dcu; 1.

KW Transport; Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 1 20
 FT DOMAIN 21 21
 FT TRANSMEM 22 40
 FT DOMAIN 41 56
 FT TRANSMEM 57 74
 FT DOMAIN 75 88
 FT TRANSMEM 89 106
 FT TRANSMEM 107 135
 FT TRANSMEM 136 150
 FT TRANSMEM 151 221
 FT TRANSMEM 232 249
 FT TRANSMEM 250 267
 FT TRANSMEM 268 285
 FT TRANSMEM 296 313
 FT TRANSMEM 314 335
 FT TRANSMEM 336 353
 FT TRANSMEM 354 358
 FT TRANSMEM 359 383
 FT DOMAIN 384 443
 SEQUENCE 443 AA: 47291 MW: ECD39D53B250449 CRC64:
 Query Match
 Best Local Similarity 91.2%; Score 31; DB 1; Length 443;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHWIP 6
 DB 171 LHWIP 176

RESULT 14

DCUA_HELPJ STANDARD: PRT: 443 AA.
 ID 025425:
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Anaerobic C4-dicarboxylate transporter dcua.
 GN DCUA OR HP0724.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26595 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
 Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 Nelson K., Quackenbush J., Zhou L., Kirness E.F., Peterson S.,
 Loftus B., Richardson D., Dodson R., Khairak H.G., Glodek A.,
 McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.R.,
 Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
 Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori."
 RL Nature 388:539-547(1997).
 CC -1- FUNCTION: RESPONSIBLE FOR THE TRANSPORT OF C4-DICARBOXYLATES FROM
 CC THE PERIPLASM ACROSS THE INNER MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein, inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE DCUA / DCUB (TC 2.A.13.1) FAMILY OF
 CC TRANSPORTERS.

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CC -----
DR EMBL: AE000585; AAD0773.1; -.
DR TIGR: HP0724; -.
DR InterPro: IPR004668; Dcu.
DR Pfam: PF03605; Dcu; 1.
DR TIGRFAMs: TIGR00770; Dcu; 1.
DR Transport: Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 1 20
FT DOMAIN 1 20
FT TRANSMEM 21 21
FT TRANSMEM 22 21
FT TRANSMEM 22 40
FT TRANSMEM 41 56
FT TRANSMEM 57 74
FT TRANSMEM 75 88
FT TRANSMEM 89 106
FT TRANSMEM 107 135
FT TRANSMEM 136 150
FT TRANSMEM 151 231
FT TRANSMEM 232 249
FT TRANSMEM 250 267
FT TRANSMEM 268 285
FT TRANSMEM 286 295
FT TRANSMEM 296 313
FT TRANSMEM 314 335
FT TRANSMEM 336 353
FT TRANSMEM 354 358
FT TRANSMEM 359 383
FT TRANSMEM 384 443
SQ SEQUENCE 443 AA; 47173 MW; 0E693630A0B50141 CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 1; Length 443;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
1:1111
Db 171 LMWIP 176

RESULT 15
KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE I9 kappa chain V-III region Vg precursor (Fragment).
DE Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the Vg locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X01668; -. NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HUVG.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR Pfam: PF00047; I9; 1.
```

```
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 115
FT DISULFID 43 108
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match
Best Local Similarity 88.2%; Score 30; DB 1; Length 115;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
1:1:1:1
Db 11 LLIWIP 16
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Search completed: January 3, 2003, 15:29:19
Job time : 6.18182 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:24:35 ; Search time 20.3182 Seconds
(without alignments)
60.846 Million cell updates/sec

Title: US-09-543-188a-3
Perfect score: 34
Sequence: 1 LLIWIP 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	157	5 Q9NFS8	Q9NFS8 plasmodium
2	34	100.0	367	16 P71056	P71056 bacillus su
3	34	100.0	554	4 Q92521	Q92521 homo sapien
4	34	100.0	554	4 Q8WV7	Q8WV7 homo sapien
5	34	100.0	754	10 Q92022	Q92022 arabidopsis
6	34	100.0	2457	5 Q77375	Q77375 plasmodium
7	33	97.1	133	16 Q985W5	Q985W5 rhizobium 1
8	33	97.1	290	17 Q8TTC2	Q8TTC2 methanosa
9	33	97.1	304	3 Q06522	Q06522 saccharomy
10	33	97.1	326	16 Q98K16	Q98K16 rhizobium 1
11	32	94.1	110	16 Q9KZB9	Q9KZB9 streptomy
12	32	94.1	138	2 Q936U1	Q936U1 pseudomon
13	32	94.1	139	2 Q05611	Q05611 pseudomon
14	32	94.1	200	16 Q9KC00	Q9KC00 bacillus ha
15	32	94.1	230	16 Q9RXX7	Q9RXX7 streptomy
16	32	94.1	269	5 Q18003	Q18003 caenorhabd1

17	32	94.1	382	10 Q8W2P6	Q8W2P6 oryza sativ
18	32	94.1	479	2 Q8VTR2	Q8VTR2 bacteroides
19	32	94.1	501	16 Q9PG13	Q9PG13 xylella fas
20	32	94.1	542	5 Q18556	Q18556 caenorhabd1
21	32	94.1	902	10 Q8S191	Q8S191 oryza sativ
22	32	94.1	3011	12 Q9D7D8	Q9D7D8 hepatitis c
23	31	91.2	100	4 Q9P0F3	Q9P0F3 homo sapien
24	31	91.2	103	4 Q9UMS9	Q9UMS9 homo sapien
25	31	91.2	131	16 Q9K321	Q9K321 bacillus ha
26	31	91.2	150	16 Q98LM8	Q98LM8 rhizobium 1
27	31	91.2	157	10 Q9C8R7	Q9C8R7 arabidopsis
28	31	91.2	159	11 Q8VD57	Q8VD57 mus musculu
29	31	91.2	186	4 Q9UMT0	Q9UMT0 mus musculu
30	31	91.2	229	5 Q19308	Q19308 caenorhabd1
31	31	91.2	280	4 Q92637	Q92637 homo sapien
32	31	91.2	298	4 Q9HD97	Q9HD97 homo sapien
33	31	91.2	299	4 Q9UBK4	Q9UBK4 homo sapien
34	31	91.2	299	4 Q9UGN4	Q9UGN4 homo sapien
35	31	91.2	301	4 Q95100	Q95100 homo sapien
36	31	91.2	330	11 Q8R142	Q8R142 mus musculu
37	31	91.2	357	6 Q8SPW5	Q8SPW5 macaca fasc
38	31	91.2	374	4 Q92663	Q92663 homo sapien
39	31	91.2	375	4 Q92495	Q92495 homo sapien
40	31	91.2	396	16 Q8X541	Q8X541 escherichia
41	31	91.2	431	16 Q9K7K1	Q9K7K1 bacillus ha
42	31	91.2	494	5 Q9N983	Q9N983 leishmania
43	31	91.2	500	16 Q8YPM6	Q8YPM6 anabaena sp
44	31	91.2	521	5 Q18267	Q18267 caenorhabd1
45	31	91.2	625	11 Q61468	Q61468 mus musculu

ALIGNMENTS

RESULT 1
Q9NFS8 PRELIMINARY: PRT: 157 AA.
AC Q9NFS8:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RNA polymerase II (Fragment).
GN RNAPOLII.
OS Plasmodium yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5861;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=265BY;
RX MEDLINE=20542027; PubMed=11087914;
RA Nivez M.P., Achbarou A., Bienvenu J.D., Mazier D., Doerig C.,
Vaquero C.;
RT "A study of selected Plasmodium yoelii messengers RNAs during
RT hepatocyte infection.";
RL Mol. Biochem. Parasitol. 111:31-39(2000).
DR EMBL, AJ271478; CAB70097.1; -;
DR InterPro: IPR000722; RNA_pol_A.
DR Pfam: PF00623; RNA_pol_A: 1.
FT NON_TER 1 157
FT NON_TER 1 157
SQ SEQUENCE 157 AA; 18667 MW; 79E0EA86CEAF5CA CRC64;

Query Match 100.0%; Score 34; DB 5; Length 157;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
| | | | |
DB 66 LLIWIP 71

RESULT 2
P71056

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ID P71056 PRELIMINARY: PRT: 367 AA.
AC P71056; O08175;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Hypothetical protein yveq.
GN yveq.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxId=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168rrp;
RA Fabret C., Quentin Y., Chapel N., Guisepi A., Halech J., Denizot F.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Denizot F.C.;
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
[3]
RC STRAIN=168;
RA MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherst S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codan J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Eutlian K.D., Ertlington J., Fabret C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-blanchard M., Klein C.,
RA Kobayashi Y., Koetler P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Puje P., Furnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
RA Saito T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tognoni A.,
RA Toseto V., Uchiyama S., Vandendol M., Vannier F., Vassarotti A.,
RA Viari A., Wambut R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=168;
RC Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z71928; CA96474.1; -.
DR EMBL: Z94043; CAB08029.1; -.
DR EMBL: Z99121; CAB15436.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 367 AA; 42554 MW; 88D37986AFD9C96 CRC64;
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Query Match 100.0%; Score 34; DB 16; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LLIWIP 6
DB 37 LLIWIP 42
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```
RESULT 3
ID 092521 PRELIMINARY: PRT: 554 AA.
AC 092521;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, last annotation update)
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97015126; PubMed=8861954;
RA Takahashi M., Inoue N., Ohishi K., Maeda Y., Nakamura N., Endo Y.,
RA Fujita T., Takeda J., Kinoshita T.;
RT "PIG-B, a membrane protein of the endoplasmic reticulum with a large
RT lumenal domain, is involved in transferring the third mannose of the
RT GPI anchor."
RL EMO J. 15:4254-4261(1996).
DR EMBL: D42138; BAA07709.1; -.
SQ SEQUENCE 554 AA; 65056 MW; B2AF87D13ADFP90B3 CRC64;
```

```
Query Match 100.0%; Score 34; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 LLIWIP 6
DB 138 LLIWIP 143
```

```
RESULT 4
ID 08WVN7 PRELIMINARY: PRT: 554 AA.
AC 08WVN7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Homo sapiens (Human).
OS Phosphatidylinositol glycan, class B.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC017711; AAH1771.1; -.
SQ SEQUENCE 554 AA; 64957 MW; E778418C02A2478 CRC64;
```

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Query Match 100.0%; Score 34; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 LLIWIP 6
DB 138 LLIWIP 143
```

```
RESULT 5
ID 092022 PRELIMINARY: PRT: 754 AA.
AC 092022;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Putative LRR receptor-linked protein kinase (Putative LRR receptor-
DE like protein kinase).
```

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GN F4C21.35 OR AF4G03390.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Habermann K., de la Bastide M., Huang E.N., Gnoc L., Schutz K.,
RA Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N.,
RA McCombie W.R.,
RT "Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cM.";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.,
RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC005275; AAD14467.1; -.
DR EMBL; AL161496; CAB77824.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002965; P_fich_extensn.
DR Pfam: PF00560; LRR; 5.
DR PRINTS; PR01217; PRICHEXTENS.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00370; LRR; 4.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 754 AA; 82315 MW; 56B5946A597F63D CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 10; Length 754;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
DB 19 LLIWIP 24

RESULT 6
ID 07375 PRELIMINARY: PRT; 2457 AA.
AC 07375.
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE DNA-directed RNA polymerase II.
GN PFC0805W, MAL3P6.20.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=3D7;
RC MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Mole S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Ruter S., Skellton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Batteil B.G.,
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum .";

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RL Nature 400:532-538(1999).
DR EMBL; Z98551; CAB1131.1; -.
DR InterPro: IPR000684; RNA_polII_repeat.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002679; RNA_pol_A2.
DR Pfam; PF00623; RNA_pol_A; 1.
DR Pfam; PF01854; RNA_pol_A2; 1.
DR PROSITE; PS00115; RNA_POL_II_REPEAT; UNKNOWN_10.
SQ DNA-directed RNA polymerase.
QY SEQUENCE 2457 AA; 278674 MW; BB0FE1135F2FF43C CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 5; Length 2457;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
DB 582 LLIWIP 587

RESULT 7
ID 0985W5 PRELIMINARY: PRT; 133 AA.
AC 0985W5.
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein mlr7498.
GN MLR7498.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFP303099; PubMed=11214968;
RT MEDLINE=21082930;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto K., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti .";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003011; BAB53588.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 133 AA; 14309 MW; E2C038E77A39DDED CRC64;

Query Match
Best Local Similarity 97.1%; Score 33; DB 16; Length 133;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
DB 93 LLIWIP 98

RESULT 8
ID 08TTC2 PRELIMINARY: PRT; 290 AA.
AC 08TTC2.
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Predicted protein.
GN MA0515.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN-C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE-21929760; PubMed-11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reece J.N., Smith K.,
 RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
 RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.M., Birren B.;
 RT "The genome of *Methanosarcina acetivorans* reveals extensive metabolic
 and physiological diversity.";
 RT Genome Res. 12:532-542(2002).
 DR EMBL: AE010712; AA03959.1; -.
 KW Complete proteome.
 SQ SEQUENCE 290 AA; 33697 MW; 931248B11C8E05CA CRC64;

Query Match
 Best Local Similarity 97.1%; Score 33; DB 17; Length 290;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6
 DB 189 LTIWIP 194

RESULT 9
 ID 006522 PRELIMINARY; PRT; 304 AA.
 AC 006522;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Chromosome XVI COSMID 9659.
 GN YPR147C OR P9659.18.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97313271; PubMed-9169875;
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
 RA Araujo R., Aparicio A., Bartell B., Badcock K., Benes V., Botstein D.,
 RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
 RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
 RA Drellis H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,
 RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
 RA Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,
 RA Johnson M., Kalman S., Kleine K., Komp C., Kudi O., Lashkari D.,
 RA Lew H., Lin A., Lin D., Louis E.U., Marathe R., Messenguy F.,
 RA Meess H.W., Milpaci S., Moestl D., Muller-Auer S., Namath A.,
 RA Nemtlich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,
 RA Punelle D., Schafer M., Scharte M., Scherens B., Schramm S.,
 RA Schroeder M., Sidic A.M., Tettein H., Urrestazu L.A., Ushinsky S.,
 RA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambolt R., Wang Y.,
 RA Wedler E., Wedler H., Winnelt E., Zhong W.W., Zollner A., Vo D.H.,
 RA Hani J.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI.";
 RT Nature 387:0-0(0).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Fulton L.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kuaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,

RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
 RA Tach A., Trevasaks E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterson R.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterson R.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 RP [5]
 RP SEQUENCE FROM N.A.
 RA Jia Y., Cherry J.M.;
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U40829; AAB68285.1; -.
 DR SGD: S0006351; YPR147C.
 DR Interpro: IPR000734; Lipase.
 DR Interpro: IPR000379; Ser_gstrs.site.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN.1.
 SQ SEQUENCE 304 AA; 34842 MW; B37EE95D46F44F34 CRC64;

Query Match
 Best Local Similarity 97.1%; Score 33; DB 3; Length 304;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6
 DB 31 LTIWIP 36

RESULT 10
 ID 098K16 PRELIMINARY; PRT; 326 AA.
 AC 098K16;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Permease protein of ribose ABC transporter.
 GN MLI1679.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MAFF303099;
 RX MEDLINE-21082930; PubMed-11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
 RT Mesorhizobium loti.
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP002998; BAB48998.1; -.
 DR Interpro: IPR001851; Bac_inmem_transp.
 KW Complete proteome.
 SQ SEQUENCE 326 AA; 34344 MW; 934FF80EDAAC8C4 CRC64;

Query Match
 Best Local Similarity 97.1%; Score 33; DB 16; Length 326;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LTIWIP 6
 DB 176 LTIWIP 181

RESULT 11
 ID 09K2H9 PRELIMINARY; PRT; 110 AA.
 AC 09K2H9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Putative integral membrane protein.
GN SC01166 OR SCG8A.20C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145.
RA Bertley S.D., Chater K.F., Cerdano-Parraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Hather N., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabinowitsch E., Rajandream M.A., Rutherford K., Ruter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
Nature 417:141-147(2002).
DR EMBL, AL33663; CAB8950.1; -
SQ SEQUENCE 110 AA; 11809 MW; C3CCFA7A44701297 CRC64;

Query Match 94.1%; Score 32; DB 16; Length 110;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
Db 68 LLIWIP 73
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RESULT 12
ID 093601 PRELIMINARY; PRT; 138 AA.
AC 093601;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical 15.1 kDa protein.
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS46-6; TRANSPOSON=TN5046;
MEDLINE=21604134; PubMed=11763242;
MINDlin S.Z., Kholodil G.Y., Gorlenko Z.M., Minakhina S.V.,
Minakhin L.S., Kalyeva E.S., Kopteva A.V., Petrova M.A.,
Yurleva O.V., Nikiforov V.G.;
"Mercury resistance transposons of Gram-negative environmental
bacteria and their classification.";
RL Res. Microbiol. 152:811-822(2001).
DR EMBL, Y18360; CAC080080.1; -
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 138 AA; 15058 MW; 132E422A81681FE5 CRC64;

Query Match 94.1%; Score 32; DB 2; Length 138;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
Db 112 LLIWIP 117
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RESULT 13
ID 005611 PRELIMINARY; PRT; 139 AA.
AC 005611;
SQ SEQUENCE 139 AA; 15114 MW; AF7F765C2C1FE5E3 CRC64;

DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Transposon Tn5041 DNA.
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KHP41; TRANSPOSON=TN5041;
MEDLINE=97419493; PubMed=9274008;
RA Kholodil G.Y., Yurleva O.V., Gorlenko Z.M., Mindlin S.Z., Bass I.A.,
Lomovskaya O.L., Kopteva A.V., Nikiforov V.G.;
"Tn5041 : a chimeric mercury resistance transposon closely related to
the toluene degradative transposon Tn4651.";
RL Microbiology 143:2549-2556(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KHP41; TRANSPOSON=TN5041;
RA Kholodil G.Y., Mindlin S.Z., Gorlenko Z.M., Bass I.A., Kalyeva E.S.,
Nikiforov V.;
"Host-dependent transposition of Tn5041.";
RL Russ. J. Genet. 36:365-373(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=KHP41; TRANSPOSON=TN5041;
RA Kholodil G.;
Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL, X98999; CAA67452.1; -
SQ SEQUENCE 139 AA; 15114 MW; AF7F765C2C1FE5E3 CRC64;

Query Match 94.1%; Score 32; DB 2; Length 139;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
Db 112 LLIWIP 117
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RESULT 14
ID 09KCU0 PRELIMINARY; PRT; 200 AA.
AC 09KCU0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical protein BHL479.
GN BHL479.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
CC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
RX Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL, AP001512; BAB05198.1; -
DR InterPro; IPR003675; ABL.
DR Pfam; PF02517; ABL; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 200 AA; 22915 MW; F793D855F156C62D CRC64;

Query Match 94.1%; Score 32; DB 16; Length 200;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
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 Db 193 LLIWIP 198

RESULT 15

O9RXX7 PRELIMINARY; PRT; 230 AA.
 AC O9RXX7;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE putative integral membrane protein.
 GN SC01418 OR SC6D7.21C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]

SEQUENCE FROM N.A.
 STRAIN-A3(2) / M145;
 Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL133213; CAB61673.1;
 SQ SEQUENCE 230 AA; 23916 MW; 5E87093F7CC1CC26 CRC64;

Query Match 94.1%; Score 32; DB 16; Length 230;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
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 Db 78 LLIWIP 83

Search completed: January 3, 2003, 15:31:56
 Job time : 22.3182 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:16 ; Search time 9 Seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-543-188a-3

Perfect score: 34

Sequence: 1 LLIWIP 6

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

al number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	91.2	20	3	US-08-996-139-16
2	31	91.2	20	4	US-08-995-659-16
3	31	91.2	20	4	US-09-215-649A-16
4	31	91.2	20	4	US-09-320-424-25
5	31	91.2	20	4	US-09-577-780-16
6	31	91.2	21	3	US-08-518-835-5
7	31	91.2	126	1	US-07-634-278-21
8	31	91.2	126	1	US-08-477-728-21
9	31	91.2	126	1	US-08-474-040-21
10	31	91.2	126	1	US-08-487-200-21
11	31	91.2	126	2	US-08-656-586-6
12	31	91.2	126	4	US-08-488-537-21
13	31	91.2	127	3	US-08-649-100-33
14	31	91.2	128	4	US-08-348-548-6
15	31	91.2	128	4	US-09-450-520A-6
16	31	91.2	128	5	PCT-US95-15716-6
17	31	91.2	131	1	US-07-634-278-67
18	31	91.2	131	1	US-08-477-728-67
19	31	91.2	131	1	US-08-474-040-67
20	31	91.2	131	1	US-08-487-200-67
21	31	91.2	131	1	US-08-137-117D-25
22	31	91.2	131	1	US-08-137-117D-33
23	31	91.2	131	2	US-08-436-717-25
24	31	91.2	131	2	US-08-436-717-35
25	31	91.2	131	2	US-08-621-751A-10
26	31	91.2	131	2	US-08-621-751A-14
27	31	91.2	131	3	US-08-589-939-3

28	31	91.2	131	3	US-08-836-561-25	Sequence 25, Appl
29	31	91.2	131	4	US-08-484-537-67	Sequence 67, Appl
30	31	91.2	131	4	US-08-579-378A-14	Sequence 16, Appl
31	31	91.2	131	4	US-08-579-378A-18	Sequence 18, Appl
32	31	91.2	132	2	US-08-379-057-16	Sequence 16, Appl
33	31	91.2	132	2	US-08-483-636-2	Sequence 2, Appl
34	31	91.2	132	2	US-08-483-636-2	Sequence 2, Appl
35	31	91.2	133	5	PCT-US93-11611-9	Sequence 9, Appl
36	31	91.2	146	2	US-08-653-402B-12	Sequence 12, Appl
37	31	91.2	219	2	US-08-902-516-2	Sequence 2, Appl
38	31	91.2	240	4	US-09-301-593-36	Sequence 36, Appl
39	31	91.2	270	4	US-09-532-856-7	Sequence 7, Appl
40	31	91.2	354	4	US-09-393-627B-28	Sequence 28, Appl
41	30	88.2	19	1	US-07-977-696C-66	Sequence 66, Appl
42	30	88.2	19	1	US-08-129-930B-66	Sequence 66, Appl
43	30	88.2	19	4	US-08-976-288A-66	Sequence 66, Appl
44	30	88.2	24	1	US-08-162-102C-27	Sequence 27, Appl
45	30	88.2	24	1	US-08-162-102C-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-16

; Sequence 16, Application US/08996139

; Patent No. 6017729

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESS: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/996,139

; FILING DATE: 22 DECEMBER 1997

; CLASSIFICATION:

; APPLICATION NUMBER: US/08/996,139

; FILING DATE: 14 OCTOBER 1997

; APPLICATION NUMBER: US/08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)567-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-996-139-16

Query Match 91.2% Score 31; DB 3; Length 20;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
DB 11 LLIWIP 16

RESULT 2

US-08-995-659-16
Sequence 16, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-16

Query Match 91.2% Score 31; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
DB 11 LLIWIP 16

RESULT 3
US-09-215-649A-16

Sequence 16, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-215-649A-16

Query Match 91.2% Score 31; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
DB 11 LLIWIP 16

RESULT 4
US-09-320-424-25
Sequence 25, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25

EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 25
LENGTH: 20
TYPE: PRF
ORGANISM: Homo sapiens
US-09-320-424-25

Query Match
Best Local Similarity 91.2%; Score 31; DB 4; Length 20;
66.7%; Pred. No. 21;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLWIP 6
11:1:1
DB 11 LLLWIP 16

SUPL 5
US-09-577-780-16
Sequence 16, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-577-780-16

Query Match
Best Local Similarity 91.2%; Score 31; DB 4; Length 20;
66.7%; Pred. No. 21;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLWIP 6
11:1:1
DB 11 LLLWIP 16

RESULT 6
US-08-518-835-5
Sequence 5, Application US/08518835
Patent No. 6017754
GENERAL INFORMATION:
APPLICANT: CHESTNUT, JONATHAN D.
APPLICANT: HOEFLE, JAMES P.
TITLE OF INVENTION: NOVEL SYSTEM FOR ISOLATING AND
IDENTIFYING EUKARYOTIC CELLS TRANSFECTED WITH GENES AND
TITLE OF INVENTION: VECTORS, HOST CELLS AND METHODS THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,835
FILING DATE: 24-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11093
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-518-835-5

Query Match
Best Local Similarity 91.2%; Score 31; DB 3; Length 21;
66.7%; Pred. No. 22;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLWIP 6
11:1:1
DB 11 LLLWIP 16

RESULT 7
US-07-634-278-21
Sequence 21, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue

CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-21

Query Match 91.2%; Score 31; DB 1; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:
DB 11 LLIWIP 16

RESULT 8

Sequence 21, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-21

Query Match 91.2%; Score 31; DB 1; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:
DB 11 LLIWIP 16

RESULT 9

US-08-474-040-21
Sequence 21, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas P.
APPLICANT: COELINGH, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-21

Query Match 91.2%; Score 31; DB 1; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
Db 11 LLLWVP 16

RESULT 10
US-08-487-200-21
Sequence 21, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-200-21

Query Match 91.2%; Score 31; DB 1; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
Db 11 LLLWVP 16

RESULT 11
US-08-656-586-6
Sequence 6, Application US/08656586
Patent No. 5834597
GENERAL INFORMATION:
APPLICANT: TSO, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,586
FILING DATE: 31-MAY-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-007210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-656-586-6

Query Match 91.2%; Score 31; DB 2; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
Db 11 LLLWVP 16

RESULT 12
US-08-484-537-21
Sequence 21, Application US/08484537
Patent No. 6180370

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
08-484-537-21

Query Match 91.2%; Score 31; DB 4; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWP 6
Db 11 LLMWP 16

RESULT 13
US-08-649-100-33
Sequence 33, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-33

Query Match 91.2%; Score 31; DB 3; Length 127;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWP 6
Db 11 LLMWP 16

RESULT 14
US-08-348-548-6
Sequence 6, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070

TELEX: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 128 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-348-548-6

Query Match 91.2%; Score 31; DB 4; Length 128;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
 11:1:1
 Db 11 LLLWVP 16

SU/T 15
 09-450-520A-6
 Sequence 6, Application US/09450520A
 Patent No. 6329511
 GENERAL INFORMATION:
 APPLICANT: Vasquez, Maximiliano
 APPLICANT: Landolfi, Nicholas F.
 APPLICANT: Tsunashita, Naoya
 APPLICANT: Queen, Cary L.
 APPLICANT: Protein Design Labs, Inc.
 TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
 FILE REFERENCE: 011823-008110US
 CURRENT APPLICATION NUMBER: US/09/450,520A
 PRIOR FILING DATE: 1998-11-29
 PRIOR APPLICATION NUMBER: 60/110,523
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 6
 LENGTH: 128
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: human-mouse
 OTHER INFORMATION: transgenic construct HuZAP VL
 US-09-450-520A-6

Query Match 91.2%; Score 31; DB 4; Length 128;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
 11:1:1
 Db 11 LLLWVP 16

Search completed: January 3, 2003, 15:34:27
 Job time : 10 secs

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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:32:11 : Search time 4.77273 Seconds
(without alignments)
23.825 Million cell updates/sec

Title: US-09-543-188a-3
Perfect score: 34
Sequence: 1 LILIIP 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues
1 number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubppaa/PCr_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	32	94.1	177	10 US-09-764-864-942	Sequence 942, App
3	31	91.2	20	9 US-09-877-650-16	Sequence 16, Appl
4	31	91.2	20	10 US-09-871-856-16	Sequence 16, Appl
5	31	91.2	80	10 US-09-894-018-97	Sequence 97, Appl
6	31	91.2	98	10 US-09-894-018-101	Sequence 101, App
7	31	91.2	106	10 US-09-894-018-95	Sequence 95, Appl
8	31	91.2	107	10 US-09-894-018-93	Sequence 93, Appl
9	31	91.2	107	10 US-09-894-018-103	Sequence 103, App
10	31	91.2	123	10 US-09-894-018-109	Sequence 109, App
11	31	91.2	128	10 US-09-881-823-14	Sequence 14, Appl
12	31	91.2	130	10 US-09-992-524-6	Sequence 6, Appl1
13	31	91.2	130	10 US-09-894-018-99	Sequence 99, Appl
14	31	91.2	131	10 US-09-286-240-2	Sequence 2, Appl1
15	31	91.2	132	9 US-09-879-461-2	Sequence 2, Appl1
16	31	91.2	134	10 US-09-881-823-2	Sequence 2, Appl1
17	31	91.2	144	10 US-09-894-018-129	Sequence 129, App
18	31	91.2	147	10 US-09-894-018-131	Sequence 131, App
19	31	91.2	148	10 US-09-894-018-127	Sequence 127, App

20	31	91.2	157	10 US-09-894-018-117	Sequence 117, App
21	31	91.2	168	10 US-09-894-018-115	Sequence 115, App
22	31	91.2	169	10 US-09-894-018-119	Sequence 119, App
23	31	91.2	180	10 US-09-894-018-125	Sequence 125, App
24	31	91.2	206	10 US-09-894-018-111	Sequence 111, App
25	31	91.2	207	9 US-10-077-438-3	Sequence 3, Appl1
26	31	91.2	207	9 US-10-077-137-3	Sequence 3, Appl1
27	31	91.2	207	9 US-10-080-797-3	Sequence 3, Appl1
28	31	91.2	211	10 US-09-894-018-85	Sequence 85, Appl
29	31	91.2	219	10 US-09-847-185-2	Sequence 2, Appl1
30	31	91.2	219	10 US-09-894-018-113	Sequence 113, App
31	31	91.2	238	9 US-09-903-327A-4	Sequence 4, Appl1
32	31	91.2	255	10 US-09-894-018-89	Sequence 89, Appl
33	31	91.2	276	10 US-09-894-018-141	Sequence 141, App
34	31	91.2	277	10 US-09-894-018-81	Sequence 81, Appl
35	31	91.2	280	10 US-09-894-018-83	Sequence 83, Appl
36	31	91.2	281	10 US-09-894-018-91	Sequence 91, Appl
37	31	91.2	288	9 US-09-895-913A-42	Sequence 42, Appl
38	31	91.2	308	10 US-09-894-018-105	Sequence 105, App
39	31	91.2	308	10 US-09-894-018-107	Sequence 107, App
40	31	91.2	399	10 US-09-925-101-1128	Sequence 1128, App
41	31	91.2	419	10 US-09-894-018-123	Sequence 123, App
42	31	91.2	446	10 US-09-792-2008-10	Sequence 10, App
43	31	91.2	446	10 US-09-792-2008-12	Sequence 12, App
44	31	91.2	456	10 US-09-894-018-121	Sequence 121, App
45	31	91.2	463	10 US-09-835-147-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-864-761-40310
Sequence 40310, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecolica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 40310
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL136308.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EST_HUMAN HIT: AW085507.1, EVALUATE 6.40e+00
OTHER INFORMATION: SWISSPROT HIT: Q80946, EVALUATE 2.60e+00
US-09-864-761-40310

Query Match 100.0%; Score 34; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
|||||
DB 48 LLIWIP 53

RESULT 2
US-09-764-864-942
Sequence 942; Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 942
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-864-942

Query Match 94.1%; Score 32; DB 10; Length 177;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
|||||
DB 35 LLIWIP 40

RESULT 3
US-09-877-650-16
Sequence 16; Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappa

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-877-650-16

Query Match 91.2%; Score 31; DB 9; Length 20;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
|||:-|
DB 11 LLIWIP 16

RESULT 4
US-09-871-856-16
Sequence 16; Application US/09871856
Patent No. US20020081720A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappa
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856

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; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US98/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: US98/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-871-856-16

Query Match          91.2%; Score 31; DB 10; Length 20;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:|
Db 11 LLIWVP 16

RESULT 5
US-09-894-018-97
; Sequence 97, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV.3s2(-3)
US-09-894-018-97

Query Match          91.2%; Score 31; DB 10; Length 80;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:|
```

```

Db 13 LLIWVP 18

RESULT 6
US-09-894-018-101
; Sequence 101, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV.PC3
US-09-894-018-101

Query Match          91.2%; Score 31; DB 10; Length 98;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:|
Db 13 LLIWVP 18

RESULT 7
US-09-894-018-95
; Sequence 95, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 106
; TYPE: PRT
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV.3s2
US-09-894-018-95

Query Match 91.2%; Score 31; DB 10; Length 106;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
DB 13 LLLWVP 18

RESULT 8
US-09-894-018-93

Sequence 93, Application US/09894018
Patent No. US20020119127A1

GENERAL INFORMATION:

APPLICANT: EPIMUNE, Inc.

APPLICANT: Sette, Alessandro

APPLICANT: Chestnut, Robert

APPLICANT: Livingston, Brian

APPLICANT: Baker, Denisw

APPLICANT: Newman, Mark

APPLICANT: Brown, David

TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING

FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION NUMBER: US/09/894, 018

PRIOR FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 93

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: HCV.3s1

US-09-894-018-93

Query Match

Best Local Similarity 91.2%; Score 31; DB 10; Length 107;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
DB 13 LLLWVP 18

RESULT 9
US-09-894-018-103

Sequence 103, Application US/09894018

Patent No. US20020119127A1

GENERAL INFORMATION:

APPLICANT: EPIMUNE, Inc.

APPLICANT: Sette, Alessandro

APPLICANT: Chestnut, Robert

APPLICANT: Livingston, Brian

APPLICANT: Baker, Denisw

APPLICANT: Newman, Mark

APPLICANT: Brown, David

TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING

FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION NUMBER: US/09/894, 018

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 103

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: HCV.PC4

US-09-894-018-103

Query Match

Best Local Similarity 91.2%; Score 31; DB 10; Length 107;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
DB 13 LLLWVP 18

RESULT 10
US-09-894-018-109

Sequence 109, Application US/09894018

Patent No. US20020119127A1

GENERAL INFORMATION:

APPLICANT: EPIMUNE, Inc.

APPLICANT: Sette, Alessandro

APPLICANT: Chestnut, Robert

APPLICANT: Livingston, Brian

APPLICANT: Baker, Denisw

APPLICANT: Newman, Mark

APPLICANT: Brown, David

TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING

FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION NUMBER: US/09/894, 018

PRIOR FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 109

LENGTH: 123

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: AOSI.K

US-09-894-018-109

Query Match

Best Local Similarity 91.2%; Score 31; DB 10; Length 123;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
11:1:1
DB 13 LLLWVP 18

RESULT 11
US-09-881-823-14

Sequence 14, Application US/09881823

Patent No. US20020068066A1

GENERAL INFORMATION:

APPLICANT: SHI, WENYUAN

APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 128
TYPE: PRT
ORGANISM: Murine
US-09-881-823-14

Query Match 91.2%; Score 31; DB 10; Length 128;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:|
DB 11 LLLWVP 16

RESULT 12
US-09-992-524-6
Sequence 6, Application US/09992524
Patent No. US20020091240A1
GENERAL INFORMATION:
APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Tsurushita, Naoya
APPLICANT: Queen, Cary L.
APPLICANT: Protein Design Labs, Inc.
TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-008110US
CURRENT APPLICATION NUMBER: US/09/992,524
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/450,520
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human-mouse
OTHER INFORMATION: transgenic construct HuZAF VL
US-09-992-524-6

Query Match 91.2%; Score 31; DB 10; Length 128;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:|
DB 11 LLLWVP 16

RESULT 13
US-09-894-018-99
Sequence 99, Application US/09894018
Patent No. US20020119127A1
GENERAL INFORMATION:
APPLICANT: EPIMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian

APPLICANT: Baker, Dennis
APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 99
LENGTH: 130
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HCV.353
US-09-894-018-99

Query Match 91.2%; Score 31; DB 10; Length 130;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:|
DB 13 LLLWVP 18

RESULT 14
US-09-286-240-2
Sequence 2, Application US/09286240
Patent No. US20020010320A1
GENERAL INFORMATION:
APPLICANT: Pett, James W
TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
FILE REFERENCE: 10498/74073
CURRENT APPLICATION NUMBER: US/09/286,240
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 131
TYPE: PRT
ORGANISM: Mus musculus
US-09-286-240-2

Query Match 91.2%; Score 31; DB 10; Length 131;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLIWIP 6
||:|:|
DB 11 LLLWVP 16

RESULT 15
US-09-879-461-2
Sequence 2, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation

STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2

Query Match 91.2%; Score 31; DB 9; Length 132;
Best Local Similarity 66.7%; Pred. NO. 71;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLIWIP 6
||:|:|
DB 11 LLLWVP 16

Search completed: January 3, 2003, 15:52:04
Job time : 4.77273 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:21:45 ; Search time 26.5909 seconds
(without alignments)
30.067 Million cell updates/sec

Title: US-09-543-188A-4

Perfect score: 44

Sequence: 1 WLWMP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	6	AAU11827	Peptide ligand for
2	42	95.5	173	ABB88811	Human polypeptide
3	40	90.9	137	AAU96472	Human reproductive
4	40	90.9	235	AAU41991	Human polypeptide
5	40	90.9	533	AAU40205	Human polypeptide
6	40	90.9	534	ABG30232	Novel human diapo
7	40	90.9	534	AAU32016	Novel human diapo
8	38	86.4	142	ABB67564	Drosophila melanog
9	38	86.4	402	AAU00427	Caenorhabditis ele
10	38	86.4	402	AAE22532	Caenorhabditis ele

11	37	84.1	27	AAU01575
12	37	84.1	384	ABP28377
13	37	84.1	385	ABB60764
14	37	84.1	393	AAU03712
15	37	84.1	415	AAU14114
16	37	84.1	415	AAU91293
17	37	84.1	458	ABP30101
18	37	84.1	461	ABBA5843
19	37	84.1	561	AAU14440
20	37	84.1	836	AAU93820
21	37	84.1	2701	AAU99850
22	36	81.8	331	AAU46431
23	36	81.8	719	ABBA7832
24	35	79.5	54	ABP31650
25	35	79.5	83	ABG37801
26	35	79.5	109	AAU87271
27	35	79.5	117	AAU89871
28	35	79.5	195	ABG10973
29	35	79.5	360	AAU35593
30	35	79.5	382	ABB76184
31	35	79.5	475	AAU34459
32	35	79.5	524	AAU74306
33	35	79.5	533	AAU33181
34	34	77.3	10	AAW32770
35	34	77.3	17	AAU16194
36	34	77.3	17	AAU68833
37	34	77.3	17	AAU58320
38	34	77.3	17	AAU09966
39	34	77.3	17	AAU17743
40	34	77.3	17	ABB72639
41	34	77.3	62	ABG01631
42	34	77.3	76	AAU50181
43	34	77.3	103	AAU24385
44	34	77.3	130	ABG01550
45	34	77.3	160	AAU43406

ALIGNMENTS

RESULT 1	
AAU11827	
AAU11827 standard; peptide: 6 AA.	
XX	
AC AAU11827;	
XX	
DT 26-MAR-2002 (first entry)	
XX	
DE Peptide ligand for Prion protein, PrP, #2.	
XX	
KW Prion protein; PrP; ligand; octapeptide motif; scrapie;	
KW Prion-associated disease; Creutzfeldt-Jakob disease;	
KW Gerstmann-Strausler-Scheinker disease; fatal familial insomnia;	
KW feline spongiform encephalopathy; bovine spongiform encephalopathy;	
KW transmissible mink encephalopathy; exotic ungulate encephalopathy;	
KW chronic wasting disease.	
XX	
OS Synthetic.	
XX	
PN WO200177687-A2.	
XX	
PD 18-OCT-2001.	
XX	
PF 05-APR-2001; 2001WO-US11150.	
XX	
PR 05-APR-2000; 2000US-0543188.	
XX	
PA (VITE-) VI TECHNOLOGIES INC.	
XX	
PI Hammond DJ, Wiltshire VR, Carbonei R, Shen H;	
XX	
DR WPI: 2002-061944/08.	
XX	

Human secreted pro
Streptococcus poly
Drosophila melanog
Group B Streptococ
Non-receptor like
Human NOV8 protein
Streptococcus poly
Listeria monocylog
Protein involved 1
Human polypeptide,
Human type 3 Inost
Propionibacterium
Listeria monocylog
Human ORF623 prote
Human peptide enco
Human signal pepti
Human Immune/haema
Novel human diapo
Haemophilus influe
Human G-protein co
E. coli cellular p
Neisseria meningit
Novel human secret
Human platelet gly
Peptide containing
Peptide binding in
IL-1R1 binding pe
Interleukin-1 type
IL-1 antagonist pe
Interleukin 1 anta
Novel human diapo
Propionibacterium
Human EST encoded
Novel human diapo
Propionibacterium

PT New ligands for prion proteins, useful for detection or removal or
PT prions and for treating prion-associated diseases, recognize a specific
PT octapeptide motif -
XX
XX

PS Claim 16; Page 34; 47pp; English.

XX The invention relates to a ligand of less than 6 kD that binds to a
CC polypeptide containing the sequence glytrylglylnprohisglygly (A) or an
CC analogue that is the retro-inverso isomer of (A). The sequence A is
CC an octapeptide motif from the prion protein (PrP). The ligands are
CC identified by binding assays with the peptide (A) or peptides containing
CC (A). The ligands are used for detecting prion proteins (or prions) in
CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jakob diseases (in
CC latrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strussler-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is a ligand of the invention.

Sequence 6 AA:

Query Match 100.0%; Score 44; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. NO. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWIP 6
DB 1 WLXWIP 6

RESULT 2
ABB89811

ID ABB89811 standard; Protein; 173 AA.

AC ABB89811;

DT 24-MAY-2002 (first entry)

DE Human polypeptide SEQ ID NO 2187.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

PN WO200190304-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US16450.

XX 19-MAY-2000; 2000US-205515P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Blirze CE, Rosen CA;

XX WPI; 2002-122018/16.

XX N-PSDB; ABL90220.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -

XX Claim 11; SEQ ID NO 2187; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABL90853) and proteins

CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 173 AA:

Query Match 95.5%; Score 42; DB 23; Length 173;
Best Local Similarity 83.3%; Pred NO. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWIP 6
DB 15 WLXWIP 20

RESULT 3
AAM96472

ID AAM96472 standard; Protein; 137 AA.

AC AAM96472;

DT 21-NOV-2001 (first entry)

DE Human reproductive system related antigen SEQ ID NO: 5130.

XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy.

XX Homo sapiens.

PN WO200155320-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01339.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225247.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235835.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.

PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251088.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-465570/50.
DR N-PSDB; AAL02442.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
XX Is used in preventing, treating or ameliorating a medical condition -
XX
Claim 11: SEQ ID NO 5130; 1297bp + Sequence Listing; English.
PS
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX
SQ Sequence 137 AA:

Query Match 90.9%; Score 40; DB 22; Length 137;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWIP 6
1:11:1
DB 114 WYRWIP 119

RESULT 4
AAM41991
ID AAM41991 standard; Protein; 235 AA.
XX

AC AAM41991;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 6922.
 XX
 KW Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 XX Homo sapiens.
 OS
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI61147.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 2; SEQ ID NO 6922; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/Inhibin activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX
 SO Sequence 235 AA;
 XX
 Query Match 90.9%; Score 40; DB 22; Length 235;
 Best Local Similarity 66.7%; Pred. No. 37;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WLWIP 6
 I::I::I
 Db 212 WYWVP 217
 RESULT 5

AAM40205
 ID AAM40205 standard; Protein; 533 AA.
 XX
 AC AAM40205;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 3350.
 XX
 KW Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 XX Homo sapiens.
 OS
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI59361.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 5; SEQ ID NO 3350; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/Inhibin activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX
 SO Sequence 533 AA;
 XX
 Query Match 90.9%; Score 40; DB 22; Length 533;
 Best Local Similarity 66.7%; Pred. No. 84;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WLWIP 6
 I::I::I
 Db 510 WYWVP 515

RESULT 6
ABG30232
ID ABG30232 standard; Protein: 534 AA.
XX
AC ABG30232;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #30223.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS94419.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 60591; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 534 AA;

Query Match 90.9%; Score 40; DB 22; Length 534;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLYWIP 6
DB 511 WYTWYP 516

RESULT 7
AAU32016
ID AAU32016 standard; Protein: 534 AA.
XX
AC AAU32016;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #2507.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dmanac RT;
XX
DR WPI: 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 541; 765bp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising
XX the nucleic acids encoding the polypeptides and cells genetically
XX engineered to express them are also useful for producing the proteins.
XX The proteins are useful in genetic vaccination, testing and
XX therapy, and can be used as nutritional supplements. They may be used to
XX increase stem cell proliferation; to regulate haematopoiesis; and in
XX bone, cartilage, tendon and/or nerve tissue growth or regeneration;
XX immune suppression and/or stimulation; as anti-inflammatory agents; and
XX in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
XX sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 534 AA;

Query Match 90.9%; Score 40; DB 22; Length 534;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLYWIP 6
DB 511 WYTWYP 516

RESULT 8
ABB67564
ID ABB67564 standard; Protein: 142 AA.
XX
AC ABB67564;
XX
DT 26-MAR-2002 (first entry)
XX

DE	Drosophila melanogaster polypeptide SEQ ID NO 29484.
XX	
KW	Drosophila: developmental biology; cell signalling; insecticide;
RW	pharmaceutical.
XX	
OS	Drosophila melanogaster.
PX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US09231.
XX	
PR	23-MAR-2000; 2000US-191637P.
XX	
PA	11-JUL-2000; 2000US-0614150.
XX	
PI	(PEKE) PE CORP NY.
PT	Venter JC, Adams M, Li PWD, Myers EW;
DR	WPI: 2001-656860/75.
N-PSDB:	ABLI1667.
PT	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signalling and cell-cell
PT	interactions -
PS	
PS	Disclosure: SEQ ID NO 29484; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	useful in developmental biology and in elucidating cell signalling and
CC	cell-cell interactions in higher eukaryotes for the development of
CC	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA
CC	sequences (ABLI01840-ABLI6175) and the encoded proteins
CC	(ABB57737-ABB2072).
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SO	Sequence 142 AA;
	Query Match 86.4%; Score 38; DB 22; Length 142;
	Best Local Similarity 83.3%; Pred. No. 48;
	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
	1 WLWIP 6
	53 WRWIP 58
RESULT 9	
AU00427	AAU00427 standard; Protein: 402 AA.
AC	AAU00427:
XX	
DT	11-MAY-2001 (first entry)
XX	
DE	Caenorhabditis elegans omega-3 fatty acyl desaturase fat-1 polypeptide.
XX	
KW	Omega-3 fatty acyl desaturase; fat-1; omega-6 fatty acid; lipid;
RW	omega-3 fatty acid; omega-3 desaturase activity; food; oil;
KM	nutritional supplement; chemical feedstock.
XX	
CS	Caenorhabditis elegans.
XX	
XX	
FH	Key Location/Qualifiers
FT	Region 80..124
FT	/note= "Region containing stretches of hydrophobic
FT	residues similar to those found in other
FT	desaturases"

FT	Misc-feature	123	/note= "Highly conserved in membrane desaturases"
FT	Misc-feature	127	/note= "Highly conserved in membrane desaturases"
FT	Misc-feature	159	/note= "Highly conserved in membrane desaturases"
FT	Misc-feature	162..163	/note= "Highly conserved in membrane desaturases"
FT	Region	229..284	/note= "Region containing stretches of hydrophobic residues similar to those found in other desaturases"
FT	Misc-feature	324	/note= "Highly conserved in membrane desaturases"
FT	Misc-feature	327..328	/note= "Highly conserved in membrane desaturases"
PN	US6194167-B1.		
PD	27-FEB-2001.		
PF	18-FEB-1998;	98US-0025578.	
PR	18-FEB-1997;	97US-0038409.	
PA	(UNIV) UNIV WASHINGTON STATE RES FOUND.		
PI	Browse JA, Spsychalla JP;		
DR	WPI: 2001-217927/22.		
DR	N-PSDB: AAS00431.		
PT	Novel host cell transformed with recombinant fat-1 polynucleotide encoding polyepit which desaturates omega-6 fatty acid to corresponding omega-3 fatty acid, useful for producing lipids	-	
PS	Claim 1; Fig 1; 17pp: English.		
XX	The present sequence represents Caenorhabditis elegans omega-3 fatty acyl desaturase fat-1 polypeptide. The polypeptide desaturates an omega-6 fatty acid to a corresponding omega-3 fatty acid by catalysing the introduction of an omega-3 double bond into 18'-, 20'-, and 22- carbon fatty acids. Recombinant expression of C. elegans fat-1 polynucleotide in a wide variety of host cells, including Arabidopsis thaliana and Saccharomyces cerevisiae, produces a polypeptide with omega-3 desaturase activity. A host cell transformed with C. elegans fat-1 polynucleotide is useful for desaturating an omega-6 fatty acid to an omega-3 fatty acid by growing the host cell under conditions under which the polypeptide is expressed. The fat-1 polypeptide is useful for producing lipids having a higher proportion of omega-3 fatty acid and the lipids are useful as food, oils, as nutritional supplements, and as chemical feedstocks.		
SSQ	Sequence	402 AA;	
OY	1 WLWTP 6		
DB	261 WYWP 266		
RESULT 10			
AAE22532			
ID	AAE22532 standard; Protein; 402 AA.		
XX	AAE22532;		
DT	26-JUL-2002 (first entry)		
XX	Caenorhabditis elegans fat-1 (omega-3 fatty acyl desaturase) protein.		

```
XX XX FAT-1 protein; omega-3 fatty acyl desaturase; chemical feedstock;
KM food oil; nutritional supplement; enzyme.
XX XX
XX XX Caenorhabditis elegans.
XX XX
XX XX US2002042933-A1.
XX XX
XX XX 11-APR-2002.
XX XX
XX XX 20-DEC-2000; 2000US-0747755.
XX XX
XX XX 18-FEB-1997; 97US-038409P.
XX XX 18-FEB-1998; 98US-0025578.
XX XX
XX XX (BROWSE J A.
XX XX (SPYC/) SPYCHALLA J P.
XX XX
XX XX Browse JA, Spychalla JP;
XX XX
XX XX MPI: 2002-361389/39.
XX XX N-PSDB; AAD35559.
XX XX
XX XX Recombinant expression of fat-1 gene of Caenorhabditis elegans in a
XX XX PT wide variety of cells, including cells of Arabidopsis thaliana and
XX XX PT Saccharomyces cerevisiae, produces a polypeptide having omega-3
XX XX PT desaturase activity -
XX XX
XX XX Example 1; Fig 1; 20pp; English.
XX XX
XX XX The present sequence is Caenorhabditis elegans FAT-1, an omega-3 fatty
XX XX CC acyl desaturase protein. FAT-1 polypeptide is useful for producing lipids
XX XX CC having a higher proportion of omega-3 fatty acid. Such lipids are useful
XX XX CC as food oils nutritional supplements and as chemical feedstocks.
XX XX
XX XX SQ Sequence 402 AA;
XX XX
XX XX Query Match 86.4%; Score 38; DB 23; Length 402;
XX XX Best Local Similarity 66.7%; Pred. No. 1.3e+02;
XX XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX QY 1 WLXWIP 6
XX XX 11:1:1
XX XX Db 261 WXYWVP 266
XX XX
XX XX RESULT 11
XX XX AAD01575
XX XX AAU01575 standard; Peptide; 27 AA.
XX XX
XX AC AAU01575;
XX XX
XX DT 18-JUL-2001 (first entry)
XX XX
XX DE Human secreted protein immunogenic epitope encoded by gene #15.
XX XX
XX XX Human secreted protein; autoimmune disorder; hyperproliferative disorder;
XX XX KM cardiovascular disorder; cerebrovascular disorder; angiogenesis;
XX XX KM nervous system disorder; bacterial infection; viral infection;
XX XX KM fungal infection; ocular disorder; wound healing; tissue regeneration;
XX XX KM epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
XX XX
XX XX Homo sapiens.
XX XX
XX XX WO200123547-A1.
XX XX
XX XX 05-APR-2001.
XX XX
XX XX 26-SEP-2000; 2000WO-US26337.
XX XX PF
XX XX 27-SEP-1999; 99US-0155806.
XX XX
XX XX (HUMA-) HUMAN GENOME SCI INC.
```

```
XX XX Komatsoulis GA, Ruben SM, Rosen CA;
XX XX PI
XX XX DR MPI: 2001-266151/27.
XX XX DR N-PSDB; AAS02654.
XX XX
XX XX Nucleic acids encoding 26 human secreted polypeptides, useful for
XX XX PT preventing, diagnosing and/or treating e.g. Gaucher's disease,
XX XX PT Alzheimer's disease, Schmitzer syndrome, Creutzfeldt-Jacob disease,
XX XX PT diabetes mellitus and multiple sclerosis -
XX XX
XX XX PS Disclosure; Page 387; 412pp; English.
XX XX
XX XX The sequence represents a human secreted protein encoded by a nucleic
XX XX CC acid of the invention. Secreted proteins and their related nucleic acids
XX XX CC can be used in the diagnosis of or susceptibility to a pathological
XX XX CC condition by determining the presence or absence of a mutation in a
XX XX CC nucleic acid or the presence or amount of expression of a secreted
XX XX CC protein. The sequences are used to prevent, treat or ameliorate a medical
XX XX CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
XX XX CC chickens or sheep. The antibodies to the polypeptides can also be used in
XX XX CC alleviating symptoms associated with disorders and in diagnostic
XX XX CC immunoassays e.g. radioimmunoassays or enzyme linkedCC immunosorbent
XX XX CC assays (ELISA). The disorders include autoimmune diseases e.g. rheumatoid
XX XX CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
XX XX CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
XX XX CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
XX XX CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
XX XX CC fungi and ocular disorders e.g. corneal infection. The peptides can also
XX XX CC be used to aid wound healing and epithelial cell proliferation, to help
XX XX CC prevent skin ageing due to sunburn, to maintain organs before
XX XX CC transplantation, to regenerate tissues, in chemotaxis and as a food
XX XX CC additive or preservative to alter storage capabilities.
XX XX
XX XX SQ Sequence 27 AA;
XX XX
XX XX Query Match 84.1%; Score 37; DB 22; Length 27;
XX XX Best Local Similarity 66.7%; Pred. No. 13;
XX XX Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 WLXWIP 6
XX XX 11:1:1
XX XX Db 8 WLWMLP 13
XX XX
XX XX RESULT 12
XX XX ABP28377
XX XX ID ABP28377 standard; Protein; 384 AA.
XX XX
XX XX AC ABP28377;
XX XX
XX DT 02-JUL-2002 (first entry)
XX XX
XX DE Streptococcus polypeptide SEQ ID NO 5930.
XX XX
XX XX Streptococcus; GAS; GBS: group B streptococcus; Streptococcus agalactiae;
XX XX KM group A streptococcus; Streptococcus pyogenes; antibacterial;
XX XX KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX XX
XX XX Streptococcus agalactiae.
XX XX
XX XX OS
XX XX PN MO200234771-A2.
XX XX
XX XX 02-MAY-2002.
XX XX
XX XX 29-OCT-2001; 2001WO-GB04789.
XX XX
XX XX 27-OCT-2000; 2000GB-0026333.
XX XX PF
XX XX 24-NOV-2000; 2000GB-0028727.
XX XX PR
XX XX 07-MAR-2001; 2001GB-0005640.
XX XX
XX XX (CHIR-) CHIRON SPA.
XX XX PA
XX XX (GENO-) INST GENOMIC RES.
```

XX Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX
DR MPI: 2002-352536/38.
DR N-PSDB: ABN69008.
XX
XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX
PS Claim 1; Page 3755; 4525pp; English.
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN6004-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX
SQ Sequence 384 AA;
XX
Query Match 84.1%; Score 37; DB 23; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLWMI 5
DB 25 WLWMI 29
XX
RESULT 13
ABN60764
ID ABB60764 standard; Protein; 385 AA.
XX
AC ABB60764;
XX
XX 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 9084.
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KM pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
DR MPI: 2001-656860/75.
DR N-PSDB: ABL04867.
XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Disclosure; SEQ ID NO 9084; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL1640-ABL16175) and the encoded proteins
CC (ABN57737-ABN72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 385 AA;
XX
Query Match 84.1%; Score 37; DB 22; Length 385;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 WLWMI 6
DB 360 WLWMI 365
XX
RESULT 14
AAU03712
ID AAU03712 standard; Protein; 393 AA.
XX
AC AAU03712;
XX
XX 12-SEP-2001 (first entry)
DT
XX
XX Group B Streptococcus antigenic protein, ID-189.
DE
XX
XX Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;
KM meningitis; neonate; antigenic; vaccine; infection; genital tract;
KM capsid polysaccharide vaccination.
XX
XX Streptococcus agalactiae.
OS
XX
PN WO200132882-A2.
XX
PD 10-MAY-2001.
XX
XX 07-SEP-2000; 2000WO-GB03437.
PF
XX
PR 07-SEP-1999; 99GB-0021125.
PR
XX
PA (MICR-) MICROBIAL TECHNIQUES LTD.
PA
PI Le Page RWF, Wells JM, Hanniffy SB;
PI
XX
DR MPI: 2001-316444/33.
DR N-PSDB: AAS07129.
XX
XX New polypeptides derived from Streptococcus agalactiae are useful to
PT provide detection of, and vaccination against, Group B Streptococcus
PT infections, particularly to prevent infection in neonates -
XX
PS Claim 1; Fig 1; 178pp; English.
XX
XX AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus
CC agalactiae) amino acid sequences of the invention. S. agalactiae is an
CC encapsulated bacterium which is a major pathogen of humans causing sepsis
CC and meningitis in neonates as well as adults. The S. agalactiae antigenic
CC polypeptides are used to vaccinate against Group B Streptococcus
CC infections, particularly to prevent infection in new born children
CC arising from the maternal genital tract. An immunogenic composition is

CC useful in the preparation of a medicament for the treatment or
 CC prophylaxis of Group B Streptococcus infection. The invention does not
 CC have the disadvantages of varied response rate associated with prior art
 CC capsid polysaccharide vaccination against Group B Streptococcus.

SQ Sequence 393 AA;

Query Match 84.1%; Score 37; DB 22; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWI 5
 |||||
 Db 99 WLXWI 103

RESULT 15

AAR14114
 ID AAR14114 standard; Protein; 415 AA.

AAR14114;

DT 09-DEC-1991 (first entry)

DE Non-receptor linked protein tyrosine phosphatase.

KW PTase; malignancy; cancer.

OS Homo sapiens.

XX Key Location/Qualifiers

FH Region 42..274

FT Active-site 377..381

FT Domain /label= nuclear recognition signal

FT 396..415

FT /label= C-terminal

FT /note= "hydrophobic"

PN WO9113989-A.

PD 19-SEP-1991.

PF 14-MAR-1991; 91WO-US01748.

PR 14-MAR-1990; 90US-0494036.

XX (WASH-) WASHINGTON RES FOUN.

XX Fischer EH, Krebs EG, Tonks NK, Cool DE;

DR WPI: 1991-295643/40.

DR N-PSDB: AAQ13802.

XX New DNA encoding non-receptor-linked protein tyrosine phosphatase

PT - used in treating malignancies associated with protein-linked

PT tyrosine phosphatase.

XX Disclosure: Fig 1; 38pp; English.

XX The sequence was deduced from a cDNA isolated from a cDNA library

CC prepd. from peripheral T cell poly(A)+ mRNA. The gene can be

CC used to express recombinant PTase or derivs. useful in cancer

CC therapy where a protein kinase is involved.

XX Sequence 415 AA:

Db 382 WLXWQP 387

Search completed: January 3, 2003, 15:28:37
 JOD time : 28.5909 secs

Query Match 84.1%; Score 37; DB 12; Length 415;

Best Local Similarity 83.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLXWIP 6
 |||||

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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:00 ; Search time 9.35455 Seconds
(without alignments)
57.944 Million cell updates/sec

Title: US-09-543-188a-4

Perfect score: 44

Sequence: 1 WLWYIP 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	95.5	3944	2 T10997	hypothetical prote
2	40	90.9	533	2 T00742	ubiquitin-binding
3	39	88.6	663	1 B54075	arachidonate 12-11
4	39	88.6	663	1 S30051	arachidonate 12-11
5	39	88.6	663	2 I52462	arachidonate 12-11
6	39	88.6	1564	2 T27121	hypothetical prote
7	38	86.4	211	2 C83360	hypothetical prote
8	38	86.4	407	2 T48817	hypothetical prote
9	38	86.4	739	2 T25030	hypothetical prote
10	37	84.1	415	1 A33899	protein-tyrosine-P
11	37	84.1	461	2 AF1079	amino acid transpo
12	37	84.1	525	2 T41427	membrane transport
13	37	84.1	938	2 S55051	Bicaudal-C - fruit
14	37	84.1	1613	2 JE0272	low density lipopr
15	37	84.1	1613	2 JE0273	low density lipopr
16	37	84.1	2701	2 C19796	inositol-trisphosp
17	36	81.8	298	2 C90880	probable phosphat
18	36	81.8	298	2 F85738	probable phosphat
19	36	81.8	340	2 A75575	probable homoprot
20	36	81.8	456	2 S47924	Mgal protein - yea
21	36	81.8	461	1 G64537	2-oxoglutarate/mal
22	36	81.8	564	1 T15477	hypothetical prote
23	36	81.8	719	2 AE1131	hypothetical prote
24	35	79.5	55	2 E82259	hypothetical prote
25	35	79.5	126	2 AG1932	hypothetical prote
26	35	79.5	136	2 AG1517	hypothetical prote
27	35	79.5	152	2 S50967	probable membrane
28	35	79.5	255	2 AE0537	hypothetical prote
29	35	79.5	264	2 S78700	probable export pr

30	35	79.5	264	2 AF0753	flagellar biosynth
31	35	79.5	269	2 T10253	membrane protein M
32	35	79.5	273	2 B83551	hypothetical prote
33	35	79.5	279	2 T10251	membrane protein M
34	35	79.5	300	2 F36790	hypothetical prote
35	35	79.5	305	2 S58822	probable membrane
36	35	79.5	360	1 A64185	phospho-N-acetylmu
37	35	79.5	371	2 H97452	cytochrome-c oxida
38	35	79.5	396	2 T25699	hypothetical prote
39	35	79.5	467	2 S49268	probable arginine
40	35	79.5	470	2 A69751	histidine permease
41	35	79.5	475	2 D64751	amino acid permeas
42	35	79.5	528	2 S26948	cytochrome-c oxida
43	35	79.5	538	2 S36424	cytochrome-c oxida
44	35	79.5	541	1 OD231	cytochrome-c oxida
45	35	79.5	541	2 A48327	cytochrome-c oxida

ALIGNMENTS

```
RESULT 1
T19997
hypothetical protein C47D12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19997
R:Gajadsky, S.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19209
A:Accession: T19997
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3944 <WIL>
A:Cross-references: EMBL:269902; PIDN:CAA93765.1; GSPDB:GN00020; CESP:C47D12.1
A:Experimental source: clone C47D12
C:Genetics:
A:Gene: CESP:C47D12.1
A:Map position: 2
A:Introns: 46/3; 308/3; 408/2; 449/3; 820/3; 946/3; 1069/1; 1634/3; 1737/2; 2009/2; 2
Query Match
Best Local Similarity 95.5%; Score 42; DB 2; Length 3944;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLWYIP 6
DB 3252 WLWYIP 3257
RESULT 2
T00742
ubiquitin-binding protein homolog A-735G6.2 - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00742
R:Adams, M.D.; Loftus, B.J.; Zhou, L.; Crosby, M.; Fuhrmann, J.; Brandon, R.; Kim, U.
Submitted to the EMBL Data Library, March 1998
A:Description: Human Chromosome 16 BAC clone CIT987SK-A-735G6.
A:Reference number: Z14181
A:Accession: T00742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-533 <ADA>
A:Cross-references: EMBL:AC002400; NID:92576344; PIDN:AAC05812.1; PID:92576346
C:Genetics:
A:Gene: A-735G6.2
A:Map position: 16p12
A:Introns: 233/1; 343/1; 412/3; 434/3; 470/1; 497/3
A:Note: A-735G6.2
Query Match
Best Local Similarity 90.9%; Score 40; DB 2; Length 533;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLYWIP 6
1111

Db 510 WLYWIP 515

RESULT 3

archidonate 12-11poxigenase (EC 1.13.11.31), leukocyte [validated] - mouse

C:Species: Mus musculus (house mouse)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: B54075; 149439
R:Chen, X.S.; Kure, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.

J. Biol. Chem. 269, 13979-13987, 1994
A:Title: CDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure

A:Reference number: A54075; MUID:94245713; PMID:8188678
A:Accession: B54075

A:Molecule type: DNA; mRNA
A:Residues: 1-663 <CHE>

A:Cross-references: GB:U04331; NID:9467216; PIDN:AAA20658.1; PID:9467217

A:Experimental source: strains C57BL/6 and ICR, spleen leukocytes
A:Note: removal or substitution of ile-663 abolished enzyme activity

R:Freire-Moar, J.; Alavi-Nassab, A.; Ng, M.; Mulkins, M.; Sigal, E.
Biochim. Biophys. Acta 1254, 112-116, 1995

A:Title: Cloning and characterization of a murine macrophage 11poxigenase.
A:Reference number: 149439; MUID:95110857; PMID:76111740

A:Accession: 149439
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-36; 'N', 38-118, 'O', 120-396, 'N', 398-663 <RES>

A:Cross-references: GB:L34570; NID:9509607; PIDN:AAA64930.1; PID:9763530

C:Comment: A second archidonate 12-11poxigenase from mouse platelets is shown in (PIR-A

C:Genetics:
A:Map position: 11

C:Superfamily: archidonate 5-11poxigenase
C:Keywords: oxidoreductase

Query Match 88.6%; Score 39; DB 1; Length 663;

Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLYWIP 6
1111

Db 551 WLYWIP 556

RESULT 4

archidonate 12-11poxigenase (EC 1.13.11.31) - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S30051
R:Matanabe, T.; Medina, J.F.; Haegstroom, J.Z.; Radmark, O.; Samuelsson, B.

Eur. J. Biochem. 212, 605-612, 1993
A:Title: Molecular cloning of a 12-11poxigenase cDNA from rat brain.

A:Reference number: S30051; MUID:93185682; PMID:8444196
A:Accession: S30051

A:Molecule type: mRNA
A:Residues: 1-663 <EMBL>

A:Cross-references: EMBL:L06040; NID:9205212; PIDN:AAA41532.1; PID:9205213

C:Superfamily: archidonate 5-11poxigenase
C:Keywords: oxidoreductase

Query Match 88.6%; Score 39; DB 1; Length 663;

Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLYWIP 6
1111

Db 551 WLYWIP 556

RESULT 5
152462
archidonate 12-11poxigenase (EC 1.13.11.31) - rat

C:Species: Rattus sp. (rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jun-1999

C:Accession: 152462
R:Hada, T.; Hagiya, H.; Suzuki, H.; Arakawa, T.; Nakamura, M.; Matsuda, S.; Yoshimoto

Biochim. Biophys. Acta 1211, 221-228, 1994
A:Title: Archidonate 12-11poxigenase of rat pineal glands: catalytic properties and

A:Reference number: 152462; MUID:94162305; PMID:8117750
A:Accession: 152462

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-663 <RES>
A:Cross-references: GB:S69383; NID:9545793; PIDN:AAB30132.1; PID:9545794

C:Superfamily: archidonate 5-11poxigenase
C:Keywords: oxidoreductase

Query Match 88.6%; Score 39; DB 2; Length 663;

Best Local Similarity 66.7%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLYWIP 6
1111

Db 551 WLYWIP 556

RESULT 6

hypothetical protein Y53C10A.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T27121
R:White, S.

Submitted to the EMBL Data Library, November 1998
A:Reference number: Z20314

A:Accession: T27121
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 11564 <EMBL>

A:Cross-references: EMBL:AL033536; PIDN:CAA22142.1; CESP:Y53C10A.9

A:Experimental source: clone Y53C10A
C:Genetics:

A:Gene: CESP:Y53C10A.9
A:introns: 43/3; 92/2; 148/2; 226/3; 354/1; 712/3; 817/1; 875/1; 916/3; 984/3; 1069/2

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 88.6%; Score 39; DB 2; Length 1564;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLYWIP 6
1111

Db 326 WLYWIP 331

RESULT 7

hypothetical protein PA2287 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83360
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L.

Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83360

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <STO>

A:Cross-references: GB:AE004654; GB:AE004091; NID:99948311; PIDN:AAG05675.1; GSPDB:GN

A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2287

Query Match 86.4%; Score 38; DB 2; Length 211;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLYWIP 6
|||:|
DB 59 WLFWIP 64

RESULT 8

T48817
hypothetical protein 68B2.10 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
C:Accession: T48817
Schulte, U.; Aign, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, R.
Submitted to the Protein Sequence Database, April 2000
Reference number: Z24541

A:Accession: T48817
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-407 <SCH>
A:Cross-references: EMBL:AL353821; GSPDB:GN00112; NCSP:68B2.10
A:Experimental source: cosmid contig 68B2; strain 74
C:Genetics:
A:Gene: NCSP:68B2.10
A:Map position: 2
A:Introns: 56/2; 68/3
C:Superfamily: Neurospora crassa hypothetical protein 68B2.10

Query Match 86.4%; Score 38; DB 2; Length 407;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLYWIP 6
|||:|
DB 172 WLFWIP 177

RESULT 9

T25030
hypothetical protein T20D3.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T25030
Alloyd, C.
Submitted to the EMBL Data Library, December 1995
Reference number: Z19971

A:Accession: T25030
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-739 <WIL>
A:Cross-references: EMBL:Z68220; PIDN:CA92491.1; GSPDB:GN00022; CESP:T20D3.11
A:Experimental source: clone T20D3
C:Genetics:
A:Gene: CESP:T20D3.11
A:Map position: 4
A:Introns: 205/1; 246/3; 437/2; 472/1; 643/3; 721/2
C:Superfamily: Caenorhabditis elegans hypothetical protein T20D3.11

Query Match 86.4%; Score 38; DB 2; Length 739;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
|||:|
DB 475 WSYWIP 480

RESULT 10

A33899
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 2 - human
N:Alternate names: protein-tyrosine-phosphatase, T-cell specific
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1990 #sequence_revision 02-May-1994 #text_change 07-May-1999
C:Accession: A33899; C60345; A45742

R:COOL, D.E.; Tonks, N.K.; Charbonneau, H.; Walsh, K.A.; Fischer, E.H.; Krebs, E.G.
Proc. Natl. Acad. Sci. U.S.A. 86: 5257-5261, 1989
A:Title: cDNA isolated from a human T-cell library encodes a member of the protein-ty
A:Reference number: A33899; MUID:89315776; PMID:2546150
A:Accession: A33899
A:Molecule type: mRNA
A:Residues: 1-415 <COO>

A:Cross-references: GB:M25393
R:Champion-Arnaud, P.; Gesnel, M.C.; Foulkes, N.; Ronsin, C.; Sassone-Corsi, P.; Brea
Oncogene 6, 1203-1209, 1991
A:Title: Activation of transcription via AP-1 or CREB regulatory sites is blocked by
A:Reference number: A60345; MUID:91319401; PMID:1650442
A:Accession: C60345
A:Status: not compared with conceptual translation

A:Molecule type: DNA
A:Residues: 348-415 <CHA>
R:Johnson, C.V.; Cool, D.E.; Glaccum, M.B.; Green, N.; Fischer, E.H.; Bruskun, A.; Hl
Genomics 16, 619-629, 1993
A:Title: Isolation and mapping of human T-cell protein tyrosine phosphatase sequences
Obs.

A:Reference number: A45742; MUID:93315152; PMID:8325634
A:Accession: A45742
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 115-125;160-170;230-241;413-415 <OH>

C:Comment: This protein and protein-tyrosine-phosphatase 11A are produced from the sa
C:Genetics:
A:Gene: GDB:PTPN2; PTP
A:Cross-references: GDB:128098; OMIM:176887
A:Map position: 18p11.22-18p11.21
A:Introns: 120/3; 165/3; 235/3; 347/2

A:Note: list of introns may be incomplete
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-ph
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyr
F:42-264/Domain: protein-tyrosine-phosphatase homology <PTP>
F:216/Active site: Cys (phosphocysteine intermediate) #status predicted
F:222/Binding site: substrate phosphate (Arg) #status predicted

Query Match 84.1%; Score 37; DB 1; Length 415;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
|||:|
DB 382 WLYWIP 387

RESULT 11

AF1079
amino acid transporter homolog lmo0037 [imported] - Listeria monocytogenes (strain EG
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1079

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maltournam, A.;
Ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-461 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAC98252.1; PID:G16409396; GSPDB:GN00177

A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmc0037

Query Match 84.1%; Score 37; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWI 5
|||||
DB 86 WLXWI 90

RESULT 12

T41427
membrane transporter - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T41427

Good, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
Submitted to the EMBL Data Library, September 1998
Reference number: 221954

A:Accession: T41427
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-525 <MOO>

A:Cross-references: EMBL:AL031798; PIDN:CAA21196.1; GSPDB:GN00068; SPDB:SPCC576.17c
A:Experimental source: strain 972h; cosmid c576

C:Genetics:
A:Gene: SPDB:SPCC576.17c

A:Map position: 3
A:Introns: 19/3

C:Superfamily: amiloride resistance protein carl

Query Match 84.1%; Score 37; DB 2; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWI 5
|||||
DB 238 WLXWI 242

RESULT 13

SS5051
Bicaudal-C - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 29-May-1998
C:Accession: SS5051

Shahone, M.; Saitman, E.E.; Lasko, P.F.
EMBO J. 14, 2043-2055, 1995

A:Title: Localized Bicaudal-C RNA encodes a protein containing a KH domain, the RNA bind

A:Reference number: SS5051; MUID:95262644; PMID:7538070

A:Accession: SS5051
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-938 <MAH>

A:Cross-references: EMBL:U15928

C:Genetics:
A:Gene: FlyBase:Bicc

A:Cross-references: FlyBase:FBgn0000182
A:Introns: 118/3; 142/1; 168/3; 277/3; 319/3; 447/1; 822/1

C:Superfamily: SAM homology
F:800-865/Domain: SAM homology <SAM>

Query Match 84.1%; Score 37; DB 2; Length 938;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWI 6
|||||
DB 30 WLXWI 35

RESULT 14

JE0272
Low density lipoprotein receptor-related protein 6 - human

C:Species: Homo sapiens (man)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Aug-2002

C:Accession: JE0272

R:Brown, S.D.; Twells, R.C.J.; Hey, P.J.; Cox, R.D.; Levy, E.R.; Soderman, A.R.; Metz
Biochem. Biophys. Res. Commun. 248, 879-888, 1998

A:Title: Isolation and characterization of LRP6, a novel member of the low density li

A:Reference number: JE0272; MUID:98369644; PMID:9704021

A:Accession: JE0272

A:Molecule type: mRNA

A:Residues: 1-1613 <BRO>

A:Cross-references: GB:AF074264; NID:93462526; PIDN:AC33006.1; PID:93462527

C:Genetics:
A:Gene: LRP6

A:Map position: 12p11-12p13

C:Superfamily: low density lipoprotein receptor-related protein; EGF homology; LDL re

F:286-323/Domain: EGF homology <EGF1>

F:592-627/Domain: EGF homology <EGF>

F:1207-1243/Domain: EGF homology <EGF2>

F:1249-1285/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:1288-1322/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:1326-1360/Domain: LDL receptor ligand-binding repeat homology <LDL3>

Query Match 84.1%; Score 37; DB 2; Length 1613;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWI 5
|||||
DB 1156 WLXWI 1160

RESULT 15
JE0273
Low density lipoprotein receptor-related protein 6 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Aug-2002

C:Accession: JE0273

R:Brown, S.D.; Twells, R.C.J.; Hey, P.J.; Cox, R.D.; Levy, E.R.; Soderman, A.R.; Metz

Biochem. Biophys. Res. Commun. 248, 879-888, 1998

A:Title: Isolation and characterization of LRP6, a novel member of the low density li

A:Reference number: JE0272; MUID:98369644; PMID:9704021

A:Accession: JE0273

A:Molecule type: mRNA

A:Residues: 1-1613 <BRO>

A:Cross-references: GB:AF074265; NID:93462528; PIDN:AC33007.1; PID:93462529

C:Genetics:
A:Gene: LRP6

A:Map position: 6

C:Superfamily: low density lipoprotein receptor-related protein; EGF homology; LDL re

F:286-323/Domain: EGF homology <EGF1>

F:592-627/Domain: EGF homology <EGF>

F:1207-1243/Domain: EGF homology <EGF2>

F:1249-1285/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:1288-1322/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:1326-1360/Domain: LDL receptor ligand-binding repeat homology <LDL3>

Query Match 84.1%; Score 37; DB 2; Length 1613;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLXWI 5
|||||
DB 1156 WLXWI 1160

Search completed: January 3, 2003, 15:33:16
Job time : 10.9545 secs

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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:22:10 ; Search time 5.18182 seconds
(without alignments)
48.025 Million cell updates/sec

Title: US-09-543-188a-4
Sequence: 1 WLXWIP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	88.6	662	1	LOX2_RAT
2	39	88.6	662	1	LOX2_RAT
3	37	84.1	415	1	CATS_MOUSE
4	37	84.1	415	1	PTN2_HUMAN
5	37	84.1	2701	1	IP3S_HUMAN
6	37	84.1	2701	1	IP3S_HUMAN
7	36	81.8	456	1	MGAL_YEAST
8	36	81.8	456	1	MGAL_YEAST
9	35	79.5	264	1	YQ21_CAEEL
10	35	79.5	300	1	FIR_SALTY
11	35	79.5	305	1	AVO1_YEAST
12	35	79.5	360	1	MRAY_HAFIN
13	35	79.5	410	1	CSG2_YEAST
14	35	79.5	467	1	MMOP_ECOLI
15	35	79.5	467	1	MMOP_ECOLI
16	35	79.5	528	1	COX1_TRIRU
17	35	79.5	538	1	COX1_RHILE
18	35	79.5	541	1	COX1_RHILE
19	35	79.5	541	1	COX1_RHILE
20	34	77.3	40	1	YB5L_PLEBO
21	34	77.3	187	1	YB18_ARCFU
22	34	77.3	268	1	TIPA_ARATH
23	34	77.3	322	1	ADP4_MOUSE
24	34	77.3	323	1	ADP4_MOUSE
25	34	77.3	323	1	ADP4_MOUSE
26	34	77.3	323	1	ADP4_MOUSE
27	34	77.3	433	1	YB1L_YEAST
28	34	77.3	619	1	VAL1_YEAST
29	34	77.3	627	1	TESK_MOUSE
30	34	77.3	821	1	HAH1_DEBOC
31	34	77.3	2164	1	CCAA_MOUSE
32	34	77.3	2212	1	CCAA_MOUSE
33	34	77.3	2212	1	CCAA_MOUSE
34	34	77.3	2216	1	YCF2_EPIVI

34	34	77.3	2222	1	CCAE_RAT	Q07652	rattus norv
35	34	77.3	2223	1	CCAE_DISOM	P56699	discopyle o
36	34	77.3	2259	1	CCAE_RABIT	O02343	oryctolagus
37	34	77.3	2272	1	CCAE_MOUSE	O61290	mus musculu
38	34	77.3	2312	1	CCAE_HUMAN	Q15878	homo sapien
39	34	77.3	2326	1	CCAB_DISOM	P56998	discopyle o
40	34	77.3	2327	1	CCAB_MOUSE	O05017	mus musculu
41	34	77.3	2336	1	CCAB_RAT	Q02294	rattus norv
42	34	77.3	2339	1	CCAB_HUMAN	O00975	homo sapien
43	34	77.3	2424	1	CCAB_RABIT	P27884	oryctolagus
44	34	77.3	2505	1	CCAA_HUMAN	O00555	homo sapien
45	34	77.3	2505	1	CCAA_HUMAN	O00555	homo sapien

ALIGNMENTS

RESULT 1	ID	LOX2_RAT	STANDARD	PRT	662 AA
AC	002759				
DT	01-JUL-1993	(Rel. 26, Created)			
DT	01-JUL-1993	(Rel. 26, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Arachidonate 12-lipoxygenase (EC 1.13.11.31) (12-LOX).				
GN	ALOX12.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN-Sprague-Dawley; TISSUE-Brain;				
RX	MEDLINE=93185682; PubMed8444196;				
RA	Watanabe T., Medina J.F., Haegstroem J.Z., Raadmark O.P.,				
RA	Samuelsson B.;				
RT	"Molecular cloning of a 12-lipoxygenase cDNA from rat brain.";				
RL	Eur. J. Biochem. 212:605-612(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Pineal gland;				
RX	MEDLINE=94162305; PubMed-8117750;				
RA	Hada T., Hagiya H., Suzuki H., Araiawa T., Nakamura M.,				
RA	Matsuda S., Yoshimoto T., Yamamoto S., Aekawa T., Morita Y.,				
RT	Ishimura K., Kim H.Y.;				
RT	"Arachidonate 12-lipoxygenase of rat pineal glands: catalytic				
RT	properties and primary structure deduced from its cDNA.";				
RL	Biochim. Biophys. Acta 1211:221-228(1994).				
CC	-1- FUNCTION: OXYGENASE AND 14,15-LEUKOTRIENE A4 SYNTHASE ACTIVITY.				
CC	-1- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-				
CC	12-hydroperoxyicoso-5,8,10,14-tetraenoate.				
CC	-1- CORFACTOR: IRON.				
CC	-1- PATHWAY: leukotrienes biosynthesis.				
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.				
CC	-1- SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY.				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL; L06040; AAA1532.1; -				
DR	EMBL; S69363; AAB30132.1; -				
DR	PIR; S30051; S30051.				
DR	HSSP; P12530; 1LOX.				
DR	InterPro; IPR000907; Lipoxygenase.				
DR	InterPro; IPR001024; Lipoxygenase_LH2.				
DR	Pfam; PF00305; Lipoxygenase; 1.				
DR	Pfam; PF01477; PLAT; 1.				
DR	PRINTS; PR00087; LIPOXYGENASE.				

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DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
KW Oxidoreductase; Dioxxygenase; Iron; Leukotriene biosynthesis.
FT INIT_MET 0
FT METAL 360 360 IRON (BY SIMILARITY).
FT METAL 365 365 IRON (BY SIMILARITY).
FT METAL 540 540 IRON (BY SIMILARITY).
FT METAL 662 662 IRON (BY SIMILARITY).
FT CONFLICT 54 54 E -> G (IN REF. 2).
FT CONFLICT 370 370 L -> V (IN REF. 2).
SQ SEQUENCE 662 AA; 75260 MW; C0187FPA27FE8F38 CRC64;

Query Match
Best Local Similarity 66.7%; Score 39; DB 1; Length 662;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLWIP 6
550 WEYWP 555

RESULT 2
LOXL_MOUSE STANDARD; PRT; 662 AA.
AC P39654;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Arachidonate 12-lipoxygenase, leukocyte-type (EC 1.13.11.31) (12-LOX).
GN ALOX12L OR ALOX15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and ICR; TISSUE=Spleen;
RX MEDLINE=94245713; PubMed=8188678;
RA Chen X.-S., Kurte U., Jenkins N.A., Copeland N.G., Funk C.D.;
RT "cDNA cloning, expression, mutagenesis of C-terminal isoleucine,
RT genomic structure, and chromosomal localizations of murine
RT 12-lipoxygenases."
RL J. Biol. Chem. 269:13979-13987(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=95110857; PubMed=7811740;
RA Freire-Moar J., Alavi-Nassab A., Ng M., Mulkins M., Sigal E.;
RT "Cloning and characterization of a murine macrophage lipoxygenase."
RL Biochim. Biophys. Acta 1254:112-116(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC CONVERTS ARACHIDONIC ACID TO 12(S)-HYDRO(PERO)XYEICOSA-TETRAENOIC
RC ACID (12-H-PETE) AND 15-HYDRO(PERO)XYEICOSA-TETRAENOIC ACID IN A 3:1
CC RATIO. CONVERTS AS WELL LINOLEIC ACID TO 13-HYDRO-
CC (PERO)XYOCTADECADIENOIC ACID.
CC -1- CATALYTIC ACTIVITY: Arachidonate + O(2) -> (5Z,8Z,10E,14Z)-(12S)-
CC 12-hydroperoxyicoso-5,8,10,14-tetraenoate.
CC -1- COFACTOR: IRON.
CC -1- PATHWAY: Leukotrienes biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: FOUND IN PITUITARY AND PINEAL GLANDS AS WELL
CC AS LEUKOCYTES, KIDNEY, AORTA, AND SMALL INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY.
CC -----
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DR EMBL; U04331; AAA20658.1; -.
DR EMBL; L34570; AAA64930.1; -.
DR HSSP; P12530; ILOX.
DR MGD; MGI:87997; Alox15.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR01024; Lipoxygenase_LH2.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
KW Oxidoreductase; Dioxxygenase; Iron; Leukotriene biosynthesis.
FT INIT_MET 0
FT METAL 360 360 IRON (BY SIMILARITY).
FT METAL 365 365 IRON (BY SIMILARITY).
FT METAL 540 540 IRON (BY SIMILARITY).
FT METAL 662 662 IRON (BY SIMILARITY).
FT CONFLICT 36 36 K -> N (IN REF. 2).
FT CONFLICT 118 118 E -> Q (IN REF. 2).
FT CONFLICT 396 396 T -> N (IN REF. 2).
SQ SEQUENCE 662 AA; 75313 MW; 5C94965B30767C2C CRC64;

Query Match
Best Local Similarity 66.7%; Score 39; DB 1; Length 662;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLWIP 6
550 WEYWP 555

RESULT 3
CATS_MOUSE STANDARD; PRT; 340 AA.
AC 070370; O54973;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cathepsin S precursor (EC 3.4.22.27).
GN CTSS OR CATS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c, and 129/Sv; TISSUE=Brain;
RA Doh-ura K.;
RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Rommelskirch W.;
RT submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 144-306 FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Cartilage;
RX MEDLINE=99326135; PubMed=10395917;
RA Soederstrom M., Salminen H., Glimmoff V., Kirschke H., Aro H.,
RA Vuorio E.;
RT "Cathepsin expression during skeletal development."
RL Biochim. Biophys. Acta 1446:35-46(1999).
RN [4]
RP SEQUENCE OF 296-340 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=98184882; PubMed=9516475;
RA Dandoy-Dron F., Guillo F., Benboudjema L., Deslys J.-P., Lasmesas C.,
RA Dormont D., Tovey M.G., Dron M.;
RT "Gene expression in scrapie. Cloning of a new scrapie-responsive gene
RT and the identification of increased levels of seven other mRNA
RT transcripts."
RL J. Biol. Chem. 273:7691-7697(1998).

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CC -1- FUNCTION: THIOLESTERASE. THE BOND-SPECIFICITY OF THIS PROTEINASE
CC IS IN PART SIMILAR TO THE SPECIFICITIES OF CATHEPSIN L AND
CC CATHEPSIN N.
CC -1- CATALYTIC ACTIVITY: Similar to cathepsin L, but with much less
CC activity on 2-Phe-Arg-1-NHMe, and more activity on the 2-Val-Val-
CC Arg-1-Xaa compound.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION FOUND
CC IN NON-SKELETAL TISSUES. RELATIVELY HIGH LEVELS FOUND IN SKELETAL
CC TISSUES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF051732; AAC05781.1; -.
CC EMBL: AF051727; AAC05781.1; JOINED.
CC EMBL: AF051728; AAC05781.1; JOINED.
CC EMBL: AF051729; AAC05781.1; JOINED.
CC EMBL: AF051726; AAC05781.1; JOINED.
CC EMBL: AF051730; AAC05781.1; JOINED.
CC EMBL: AF051731; AAC05781.1; JOINED.
CC EMBL: AF038546; AAB94925.1; -.
CC EMBL: AJ002386; CAA05360.1; -.
CC EMBL: Y18466; CAA7184.1; -.
CC EMBL: AJ23208; CAA1182.1; -.
CC HSP: P25774; IBBX.
CC MEROPS: C01.034; Cts.
CC MGD: MG1.107341; Cts.
CC InterPro: IPR000668; Peptidase_C1.
CC InterPro: IPR000169; SHProl_acsite.
CC Pfam: PF00112; Peptidase_C1; 1.
CC PRINTS: PR00705; PAPA1N.
CC Prodom: PD000158; Peptidase_C1; 1.
CC PROSITE: PS00139; THIOLESTERASE_CYS; 1.
CC PROSITE: PS00639; THIOLESTERASE_HIS; 1.
CC PROSITE: PS00640; THIOLESTERASE_ASX; 1.
CC KEGG: K01001; Thiol protease; Lysosome; Zymogen; Signal.
CC FT SIGNAL 1 17
CC FT PROPEP 18 112
CC FT CHAIN 113 340
CC FT ACT_SITE 147 147
CC FT ACT_SITE 287 287
CC FT ACT_SITE 307 307
CC FT DISULFID 134 233
CC FT DISULFID 144 189
CC FT DISULFID 178 232
CC FT DISULFID 281 329
CC FT CARBOHYD 120 120
CC FT VARIANT 218 218
CC FT CONFLICT 1 29
CC FT CONFLICT 34 34
CC FT CONFLICT 97 97
CC FT CONFLICT 106 106
CC FT CONFLICT 146 146
CC FT CONFLICT 146 146
CC SQ SEQUENCE 340 AA; 38438 MW; 068B61126E2E0C6 CRC64;
Query Match 84.1%; Score 37; DB 1; Length 340;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLYWIP 6
Db 11 WLFWMP 16
RESULT 4

PTN2_HUMAN
ID PTN2_HUMAN STANDARD; PRT; 415 AA.
AC P17706; O96H82;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 2 (BC 3.1.3.48) (T-
DE cell protein-tyrosine phosphatase) (TCPTP).
GN PTN2 OR PTP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE-T-cell;
RX MEDLINE=9315776; PubMed=2546150;
RA Cool D., Tonks N., Chardonneau H., Walsh K., Fischer E.H., Krebs E.G.;
RT "CDNA isolated from a human T-cell library encodes a member of the
RT protein-tyrosine-phosphatase family.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5257-5261(1989).
RN [2]
RP SOURCE FROM N.A.
RX MEDLINE=92115688; PubMed=1731319;
RA Mosinger B. Jr., Tillmann U., Westphal H., Tremblay M.L.;
RT "Cloning and characterization of a mouse cDNA encoding a cytoplasmic
RT protein-tyrosine-phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:499-503(1992).
RN [3]
RP SOURCE FROM N.A. (ISOFORM PTPB).
RC TISSUE-Eye;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: PTPA AND PTPB (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PTPA ISOFORM IS PROBABLY THE MAJOR PTP
CC EXPRESSED IN HUMAN TISSUES. PTPB ISOFORM WAS FOUND IN T-CELLS AND
CC IN PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
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CC -----
CC EMBL: M25393; AAA65997.1; -.
CC EMBL: M81478; -. NOT_ANNOTATED_CDS.
CC EMBL: BC008244; AAB08244.1; -.
CC EMBL: A33899; A33899.
CC HSP: P18031; LPTV.
CC Genew: HGNC:9650; PTPN2.
CC MIM: 176887; -.
CC InterPro: IPR000387; Tyr_P.
CC InterPro: IPR000242; Tyr_PP.
CC Pfam: PF00102; Y-phosphatase; 1.
CC PRINTS: PR00700; PRTYPPHPTASE.
CC SMART: SM00194; PTPC; 1.
CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
CC KEGG: K01001; T-cell; Alternative splicing.
CC FT DOMAIN 42 286
CC FT ACT_SITE 216 216
CC FT VARSPLIC 382 415
CC FT TDR (IN ISOFORM PTPA).
CC SQ SEQUENCE 415 AA; 48528 MW; 0599694A4A0508E68 CRC64;
TDR (IN ISOFORM PTPB).
PRL

Query Match 84.1% Score 37; DB 1; Length 415;
Best Local Similarity 83.3% Pred. No. 28;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLWMP 6
DB 382 WLWMP 387

RESULT 5
IP3S_HUMAN STANDARD; PRT; 2701 AA.
ID IP3S_HUMAN
AC 014571; 094773;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-
trisphosphate receptor) (Type 2 InsP3 receptor) (IP3 receptor isoform
2) (InsP3R2).
ITPR2.
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=94363219; PubMed=8081773;
RA Yamamoto-Hino M., Sugiyama T., Hikita K., Mattei M.-G.,
Hasegawa K., Sekine S., Sakurada K., Miyawaki A., Furutachi T.,
RA Hasegawa M., Mikoshiba K.;
RT "Cloning and characterization of human type 2 and type 3 inositol
1,4,5-trisphosphate receptors.";
RT Recept. Channels 2:9-22(1994).
RL [2]
RN SEQUENCE FROM N.A. (SHORT ISOFORM).
RP TISSUE=Heart;
RC MEDLINE=98399819; PubMed=9729462;
RA Futatsugi A., Kuwajima G., Mikoshiba K.;
RT "Muscle-specific mRNA isoform encodes a protein composed mainly of the
N-terminal 175 residues of type 2 Ins(1,4,5)P3 receptor.";
RL Biochem. J. 334:559-563(1998).
CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
reticulum.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM/TPR; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND IN SKELETAL MUSCLE
AND HEART.
CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
CC -1- MISCELLANEOUS: CALCIUM APPEARS TO INHIBIT LIGAND BINDING TO THE
RECEPTOR, MOST PROBABLY BY INTERACTING WITH A DISTINCT
CALCIUM-BINDING PROTEIN WHICH THEN INHIBITS THE RECEPTOR.
CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
CC -----
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CC -----
CC EMBL: D26350; BAA05384.1;
CC EMBL: AB012610; BAA33961.1;
CC DR GenBank: U00144; ITPR2.
CC MIM: 600144;

DR InterPro: IPR000699; Ca-rel_channel.
DR InterPro: IPR001682; Ca/Na_pore.
DR InterPro: IPR000493; InsP3_receptor.
DR InterPro: IPR000636; M+channel_n19.
DR InterPro: IPR003608; MIR.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF01365; Rydr_IPPR_2.
DR Pfam: PF02815; MIR_4.
DR PRINTS: PR00779; INSP3RECEPTR.
DR SMART: SM00472; MIR_4.
KW Receptor; Transmembrane; Glycoprotein; Phosphorylation;
KW Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel;
KW Alternative splicing.
FT DOMAIN 1 2227 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2228 2248 POTENTIAL.
FT DOMAIN 2249 2260 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2261 2281 POTENTIAL.
FT DOMAIN 2282 2307 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2308 2328 POTENTIAL.
FT DOMAIN 2329 2351 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2352 2372 POTENTIAL.
FT DOMAIN 2373 2394 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2395 2415 POTENTIAL.
FT DOMAIN 2416 2521 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2522 2542 POTENTIAL.
FT MOD_RES 2543 2701 CYTOPLASMIC (POTENTIAL).
FT VARSPIC 176 181 PHOSPHORYLATION (POTENTIAL).
FT VARSPIC 182 2701 IYVGRK -> DASFWI (IN SHORT ISOFORM).
SQ SEQUENCE 2701 AA; 308074 MW; EB5C7DDDD17F7A4 CRC64;

Query Match 84.1% Score 37; DB 1; Length 2701;
Best Local Similarity 100.0% Pred. No. 1,6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMI 5
DB 694 WLWMI 698

RESULT 6
IP3S_RAT STANDARD; PRT; 2701 AA.
ID IP3S_RAT
AC P29995; 099P56;
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-
trisphosphate receptor) (Type 2 InsP3 receptor) (IP3 receptor isoform
2) (InsP3R2).
GN ITPR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A. AND VARIANTS.
RC TISSUE=Brain;
RX MEDLINE=92007769; PubMed=1655411;
RA Suedhof T.C., Newton C.A., Archer B.T. III, Usinkaryov Y.A.,
RA Mignery G.A.;
RT "Structure of a novel InsP3 receptor.";
RL EMBL J. 10:3199-3206(1991).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;
RC Magnino F., Dufour J.-F.;
RT "New rat IP3R isoform 2 sequence.";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

```

CC reticulum.
CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC -1- PHM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
CC -----
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CC -----
DR EMBL: X61677: CAA43852.1: -
DR EMBL: AF329470: AAK11622.1: -
DR PIR: S17796: S17796.
DR InterPro: IPR000699: Ca-rel_channel.
DR InterPro: IPR001682: Ca/Na_pore.
DR InterPro: IPR000493: INSP3_receptor.
DR InterPro: IPR000636: M-channel_n19.
DR InterPro: IPR003608: MTR.
DR Pfam: PF00520: Ion_trans; 1.
DR Pfam: PF01365: RYDR_ITPR; 2.
DR Pfam: PF02815: MTR; 4.
DR PRINTS: PR00779: INSP3RECEPT.
DR SMART: SM00472: MIR; 4.
DR Receptor: Transmembrane; Phosphorylation; Endoplasmic reticulum;
DR Ionic channel; Ion transport; Calcium channel; Polymorphism.
KW DOMAIN 1 2227
FT TRANSSEM 2228 2248 POTENTIAL.
FT TRANSSEM 2249 2260 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 2261 2281 POTENTIAL.
FT DOMAIN 2282 2284 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 2285 2305 POTENTIAL.
FT DOMAIN 2306 2307 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 2308 2328 POTENTIAL.
FT DOMAIN 2329 2351 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 2352 2372 POTENTIAL.
FT DOMAIN 2373 2394 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 2395 2415 POTENTIAL.
FT DOMAIN 2416 2521 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 2522 2542 POTENTIAL.
FT DOMAIN 2543 2701 EXTRACELLULAR (POTENTIAL).
FT MOD_RES 2607 2607 PHOSPHORYLATION (POTENTIAL).
FT VARIANT 689 689 D -> H.
FT VARIANT 1013 1013 G -> C.
FT VARIANT 1256 1256 L -> P.
FT VARIANT 2384 2384 V -> I.
FT VARIANT 2694 2694 E -> V.
FT CONFLICT 119 119 K -> N (IN REF. 2).
FT CONFLICT 344 344 H -> R (IN REF. 2).
FT CONFLICT 943 943 W -> V (IN REF. 2).
FT CONFLICT 1692 1692 S -> G (IN REF. 2).
FT CONFLICT 2556 2556 K -> E (IN REF. 2).
SQ SEQUENCE 2701 AA; 307054 MW; 42BF7F1024335584 CRC64;

Query Match 84.1%; Score 37; DB 1; Length 2701;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MGAI protein.
CN MGAI OR YGR249W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA16-1-4;
RA Wada H.;
RL Submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=97279234; PubMed=9133742;
RA Feroli F., Carignani G., Pavanello A., Guerreiro P., Azevedo D.,
RA Rodrigues-Pousada C., Melchiorre P., Panzeri L.,
RA Agostoni Carbone M.L.;
RT "Analysis of a 17.9 kb region from Saccharomyces cerevisiae
RT chromosome VII reveals the presence of eight open reading frames,
RT including BRF1 (YFI1B70) and GCN5 genes."
RL Yeast 13:373-377(1997).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE HSF FAMILY.
CC -----
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CC -----
DR EMBL: D29626: BAA06105.1: -
DR EMBL: Y07703: CAA68970.1: -
DR EMBL: Z73034: CAA97278.1: -
DR HSP: P22121: 2HTS.
DR TRANSFAC: T03496: -
DR SGD: S0003481: MGAI.
DR InterPro: IPR000232: HSF_DNA_bind.
DR InterPro: IPR002341: HSF_FTS.
DR Pfam: PF00447: HSF_DNA_bind; 1.
DR PRINTS: PR001788: HSPDOMAIN.
DR PRODOM: PD001788: HSF_DNA_bind; 1.
DR SMART: SM00415: HSF; 1.
DR PROSITE: PS00434: HSF_DOMAIN; 1.
KW Nuclear protein; DNA-binding.
FT DNA_BIND 3 118 BY SIMILARITY.
FT DOMAIN 182 185 POLY-GLN.
FT DOMAIN 283 290 POLY-GLN.
SQ SEQUENCE 456 AA; 50735 MW; 48A21F0D89749BA6 CRC64;

Query Match 81.8%; Score 36; DB 1; Length 456;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

OY 1 WLWWT 5
DB 694 WLWWT 698

RESULT 7
MGAI_YEAST STANDARD: PRT; 456 AA.
AC P53050.
DT 01-OCT-1996 (Rel. 34, Created)

```

```

OY 1 WLWWT 6
DB 22 WLWWT 27

RESULT 8
YQ21_CAEEL
ID YQ21_CAEEL STANDARD: PRT; 564 AA.
AC Q09231;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 63.8 kDa protein C09P5.1 in chromosome III.
C09P5.1.
OS Caenorhabditis elegans.

```

CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Connell M.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO C.ELEGANS W01C9.3.
 CC -----
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 CC -----
 CC DR EMBL; U22832; AAA64509.1; -;
 CC MORNPEP; C09F5.1; CE01773.
 CC Hypothetical protein.
 CC SEQUENCE 564 AA: 63824 MW: 04A2DSACFBCT5EID CRC64;
 CC
 CC Query Match 81.8%; Score 36; DB 1; Length 564;
 CC Best Local Similarity 66.7%; Pred. No. 54;
 CC Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Oy 1 WLWTP 6
 CC Db 539 WWMWP 544
 CC
 CC RESULT 9
 CC FLIR_SALTY
 CC ID FLIR_SALTY STANDARD: PRT: 264 AA.
 CC AC P34702;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Flagellar biosynthetic protein flir.
 CC GN FLIR OR FLAP OR STM1981.
 CC OS Salmonella typhimurium.
 CC CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC CC Salmonella.
 CC OX NCBI_Taxid=602;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC STRAIN-LT2;
 CC MEDLINE=97464436; PubMed=9324257;
 CC Ohnishi K., Fan F., Schoenhals G.J., Kihara M., Macnab R.M.;
 CC "The FljO, FljP, FljQ, and Flir proteins of Salmonella typhimurium:
 CC putative components for flagellar assembly.";
 CC RT J. Bacteriol. 179:6092-6099(1997).
 CC RL [2]
 CC RN SEQUENCE FROM N.A.
 CC RP STRAIN-LT2 / SGSC1412 / ATCC 700720;
 CC RX MEDLINE=21534948; PubMed=11677609;
 CC McCalland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 CC Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D.,
 CC Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 CC Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 CC Waterston R., Wilson R.K.;
 CC "Complete genome sequence of Salmonella enterica serovar Typhimurium
 CC LT2.";
 CC RT Nature 413:852-856(2001).
 CC RL Nature 413:852-856(2001).
 CC CC -1- FUNCTION: ROLE IN FLAGELLAR BIOSYNTHESIS.
 CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC CC -1- SIMILARITY: BELONGS TO THE FLIR/MOPE/SPAR FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; L49021; AAB81321.1; -;
 CC DR EMBL; AE008787; AAL20893.1; -;
 CC DR StyGene; SG10579; flir.
 CC DR InterPro; IPR002010; Bac_export_1.
 CC DR Pfam; PF01311; Bac_export_1; 1.
 CC KW Flagella; Transmembrane; Inner membrane; Complete proteome.
 CC FT TRANSMEM 45 65 POTENTIAL.
 CC FT TRANSMEM 66 86 POTENTIAL.
 CC FT TRANSMEM 131 151 POTENTIAL.
 CC FT TRANSMEM 175 195 POTENTIAL.
 CC FT TRANSMEM 213 233 POTENTIAL.
 CC FT CONFLICT 24 24 L->R (IN REF. 1).
 CC SO SEQUENCE 264 AA: 28925 MW: 7AFF46906147A63F CRC64;
 CC
 CC Query Match 79.5%; Score 35; DB 1; Length 264;
 CC Best Local Similarity 80.0%; Pred. No. 38;
 CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Oy 1 WLWTP 5
 CC Db 9 WLMWL 13
 CC
 CC RESULT 10
 CC VG41_HSV11
 CC ID VG41_HSV11 STANDARD: PRT: 300 AA.
 CC AC Q00017;
 CC DT 01-DEC-1992 (Rel. 24, Created)
 CC DT 01-DEC-1992 (Rel. 24, Last sequence update)
 CC DT 01-DEC-1992 (Rel. 24, Last annotation update)
 CC DE Hypothetical gene 41 protein.
 CC GN 41.
 CC OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
 CC CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC CC Ictalurid Herpes-like viruses.
 CC OX NCBI_Taxid=10401;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-Auburn 1;
 CC RX MEDLINE=92087490; PubMed=1727613;
 CC RA Davison A.J.;
 CC RT "Channel catfish virus: a new type of herpesvirus.";
 CC RL Virology 186:9-14(1992).
 CC CC -----
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 CC -----
 CC DR EMBL; M75136; AAA89144.1; -;
 CC DR PIR; F36790; F36790.
 CC KM Hypothetical protein.
 CC SO SEQUENCE 300 AA: 33892 MW: D3179E15F0F3A6D CRC64;
 CC
 CC Query Match 79.5%; Score 35; DB 1; Length 300;
 CC Best Local Similarity 66.7%; Pred. No. 43;
 CC Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Oy 1 WLWTP 6
 CC Db 57 WWMWP 62
 CC
 CC RESULT 11
 CC AOY1_YEAST
 CC ID AOY1_YEAST STANDARD: PRT: 305 AA.

AC P53386; 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aquaporin-like protein AQP1.
GN AQP1 OR YP192W OR P9677.5.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoorge W.,
RA Ararajo R., Aparicio A., Barrell B.G., Badcock K., Bene V.,
RA Bosten D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Dilius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA Hunke-Smith S., Hyman R., Johnston M., Kalman S., Kaine K.,
RA Komp C., Kurd O., Lastkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Miltipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schaefer M., Scharif M.,
RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA Walsh S.V., Zambur R., Wang Y., Wedler H., Wiedler H., Winnett E.,
RA Zhong W.W., Zolnier A., Vo D.H., Hanl J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105(1997).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=96438534; PubMed=9765289;
RA Bonhivers M., Cardrey J.M., Gould S.J., Agre P.;
RT "Aquaporins in Saccharomyces. Genetic and functional distinctions
RT between laboratory and wild-type strains.";
RL J. Biol. Chem. 273:27565-27572(1998).
CC -1- FUNCTION: WATER-SPECIFIC CHANNEL. SEEMS TO BE NONFUNCTIONAL IN
CC LABORATORY STRAINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (NC 1.A.8).
CC
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CC
CC EMBL: U25841; AAB64621.1; -
DR HSSP: P29972; IFOY.
DR SGD: S0006396; AQP1.
DR InterPro: IPR000425; MIP_family.
DR Pfam: PF00230; MIP; 1.
DR ProDom: PD000295; MIP_family; 1.
DR TIGRFAMS: TIGR00861; MIP; 1.
DR PROSITE: PS00221; MIP; 1.
DR TransPort: Transmembrane.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 204 224 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT VARIANT 121 121 M -> V (IN WILD STRAINS).
FT VARIANT 121 121 T -> P (IN WILD STRAINS).
FT VARIANT 255 255
SQ SEQUENCE 305 AA; 32712 MW; 2C02491CF33AC7F CRC64;
Query Match 79.5%; Score 35; DB 1; Length 305;
Best Local Similarity 80.0%; Pred. No. 44;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 WITWI 5
Db 249 WITWI 253
RESULT 12
ID MRAY_HAETIN STANDARD; PRT; 360 AA.
AC P45062;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospho-N-acetylmuramoyl-pentapeptide transferase (EC 2.7.8.13) (UDP-
DE MurNAc-pentapeptide phosphotransferase).
GN MRAY OR H1135.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OC NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischnann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Metrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uiterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georgagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: FIRST STEP OF THE LIPID CYCLE REACTIONS IN THE
CC BIOSYNTHESIS OF THE CELL WALL. PEPTIDOGLYCAN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-L-
CC lysyl-D-alanyl-D-alanine + undecaprenyl phosphate = UDP + N-
CC acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine-
CC diposphundecaprenol.
CC -1- PATHWAY: Peptidoglycan biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 4. MRAY
CC SUBFAMILY.
CC
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CC
CC EMBL: U32793; AAC22790.1; -
DR TIGR: H1135; -
DR InterPro: IPR000715; Glycos_transf_4.
DR Pfam: PF00953; Glycos_transf_4; 1.
DR TIGRFAMS: TIGR00445; mray; 1.
DR PROSITE: PS01347; MRAY_1; 1.
DR PROSITE: PS01348; MRAY_2; 1.
DR Peptidoglycan synthesis; Cell division; Transferase; Transmembrane;
KW Complete proteome.
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 73 93 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 132 152 POTENTIAL.
FT TRANSMEM 168 188 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 239 259 POTENTIAL.

RA Mizuno T., Makino K., Nakata A., Yura T., Sampedo G., Mizobuchi K.;
 RT "Systematic sequencing of the *Escherichia coli* genome: analysis of the
 4.0 - 6.0 min (189,987 - 281,416bp) region."
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
 RA Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kundi O.,
 RA Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
 RA Davis R.W.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP POSSIBLE FUNCTION.
 RX MEDLINE=99102233; PubMed=9882684;
 RA Thambichler M., Neuhiel B., Boeck A.;
 RL "S-methylmethionine metabolism in *Escherichia coli*."
 CC J. Bacteriol. 181:662-665(1999).
 CC -1- FUNCTION: TRANSPORTER FOR THE INTAKE OF S-METHYLMETHIONINE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 (Potential).
 CC -1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
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 CC
 CC EMBL: AE000134; AAC73363.1; ALT_INIT.
 DR EMBL: DB3536; BAA77928.1; ALT_INIT.
 DR EMBL: U70214; AAB08681.1; ALT_INIT.
 DR EcoGene: EG33342; mmup.
 DR InterPro: IPR002293; AA/re_l_pmease1.
 DR InterPro: IPR004840; AAC-permease.
 DR InterPro: IPR004841; Permease.
 DR Pfam: PF00324; aa-permeases; 1.
 DR PROSITE: PS00218; AMINO ACID PERMEASE; 1.
 DR KM Transport; Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 20 40
 FT TRANSMEM 43 63 POTENTIAL.
 FT TRANSMEM 96 116 POTENTIAL.
 FT TRANSMEM 125 145 POTENTIAL.
 FT TRANSMEM 161 181 POTENTIAL.
 FT TRANSMEM 206 226 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 282 302 POTENTIAL.
 FT TRANSMEM 337 357 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 408 428 POTENTIAL.
 FT TRANSMEM 434 454 POTENTIAL.
 SQ SEQUENCE 467 AA: 50525 MW: E7ADB9A3B03C10F8 CRC64;
 Query Match 79.5%; Score 35; DB 1; Length 167;
 Best Local Similarity 80.0%; Pred. No. 65;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WLWY 5
 DB 97 WLWY 101
 RESULT 15
 ID ROCE_BACSU STANDARD; PRT; 467 AA.
 AC P39137;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Amino-acid permease roce.
 GN ROCE.
 OS *Bacillus subtilis*.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxId=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RC MEDLINE=95311309; PubMed=7540694;
 RA Gardan R., Rapoport G., Debarouille M.;
 RT "Expression of the roceDEF operon involved in arginine catabolism in
Bacillus subtilis."
 RL J. Mol. Biol. 249:843-856(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
 RT "36kb sequence between gntZ and trnY of *B. subtilis* genome."
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 RA Gilm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kunano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber V., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portelle D., Portwoll S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield C.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Togonni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vanier F., Vassarotti A.,
 RA Viari A., Wambolt R., Wedler E., Wedler H., Weitzmeyer T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zumbstein A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*."
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: PUTATIVE TRANSPORT PROTEIN INVOLVED IN ARGININE
 DEGRADATIVE PATHWAY. PROBABLY TRANSPORTS ARGININE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- INDUCTION: EXPRESSION IS SIGMA L DEPENDENT, INDUCED BY ARGININE,
 CC ORNITHINE OR PROLINE.
 CC -1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 CC EMBL: X81802; CA57399.1;
 DR EMBL: D78193; BAA11292.1;
 DR EMBL: Z99124; CAB16070.1;
 DR SdbList: BG10933; roce.
 DR InterPro: IPR002293; AA/re_l_pmease1.
 DR InterPro: IPR004840; AAC-permease.
 DR InterPro: IPR004841; Permease.

DR Pfam: PF00324; aa_permeases; 1.
 DR PROSITE: PS00218; AMINO-ACID_PERMEASE_1; 1.
 KW Transport; Amino-acid transport; Transmembrane; Complete proteome.
 FT TRANSMEM 21 41 POTENTIAL.
 FT TRANSMEM 47 67 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 162 182 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 283 303 POTENTIAL.
 FT TRANSMEM 336 356 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 409 429 POTENTIAL.
 FT TRANSMEM 435 455 POTENTIAL.
 SQ SEQUENCE 467 AA: 51634 MW: 114522C03134E6C2 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 467;
 Best Local Similarity 80.0%; Pred. No. 65;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 WLYWI 5
 98 WLYWL 102

Search completed: January 3, 2003, 15:29:20
 Job time : 6.18182 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:24:35 ; Search time 20.3182 seconds
(without alignments)
60.846 Million cell updates/sec

Title: US-09-543-188a-4
Perfect score: 44
Sequence: 1 WLXWIP 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	95.5	3944	5	Q18667
2	40	90.9	309	11	Q9D029
3	40	90.9	533	4	Q14562
4	39	88.6	1564	5	Q9XM49
5	38	86.4	71	16	Q8XZU8
6	38	86.4	142	5	Q9V596
7	38	86.4	211	16	Q9I118
8	38	86.4	402	5	Q21056
9	38	86.4	402	5	Q9NEO0
10	38	86.4	564	5	Q9ETZ3
11	38	86.4	739	5	Q01260
12	38	86.4	739	16	Q98GK3
13	37	84.1	68	11	Q64622
14	37	84.1	322	13	Q9IB44
15	37	84.1	340	11	Q99M14
16	37	84.1	385	5	Q9W3V0

17	37	84.1	406	11	Q922E7	Q922E7 mus musculus
18	37	84.1	427	10	Q93YN4	Q93YN4 arabidopsis
19	37	84.1	438	17	Q96XR2	Q96XR2 sulfobolus
20	37	84.1	461	16	Q8YAS6	Q8YAS6 listeria mo
21	37	84.1	491	10	Q9FMR7	Q9FMR7 arabidopsis
22	37	84.1	525	3	Q74899	Q74899 schizosach
23	37	84.1	561	17	Q9HKV9	Q9HKV9 thermoplasm
24	37	84.1	1476	5	Q965D3	Q965D3 dictyostell
25	37	84.1	1476	5	Q8ST66	Q8ST66 dictyostell
26	37	84.1	1613	4	Q75581	Q75581 homo sapien
27	37	84.1	1613	11	Q88572	Q88572 mus musculus
28	37	84.1	2701	6	Q8WN96	Q8WN96 bos taurus
29	36	81.8	174	12	Q8OLP7	Q8OLP7 mamestra co
30	36	81.8	218	16	Q9CJRS	Q9CJRS pasteurella
31	36	81.8	252	4	Q9H4J9	Q9H4J9 homo sapien
32	36	81.8	298	16	Q8X9S3	Q8X9S3 escherichia
33	36	81.8	340	16	Q9RYT4	Q9RYT4 mycoplasma
34	36	81.8	688	9	Q9FZR2	Q9FZR2 mycoplasma
35	36	81.8	719	16	Q8Y9S1	Q8Y9S1 listeria mo
36	36	81.8	1191	3	Q42765	Q42765 candida alb
37	35	79.5	55	16	Q9KTP6	Q9KTP6 vibrio chol
38	35	79.5	126	16	Q8Y4Z2	Q8Y4Z2 arabidopsis
39	35	79.5	136	16	Q92DY2	Q92DY2 listeria in
40	35	79.5	152	3	Q12302	Q12302 saccharomyc
41	35	79.5	161	8	Q35341	Q35341 podosporea a
42	35	79.5	179	16	Q99Q08	Q99Q08 streptomyce
43	35	79.5	228	17	Q8ZV94	Q8ZV94 pyrobaculum
44	35	79.5	255	16	Q8Z962	Q8Z962 salmonella
45	35	79.5	260	16	Q8XTJ4	Q8XTJ4 ralstonia s

ALIGNMENTS

RESULT 1
Q18667 PRELIMINARY; PRT; 3944 AA.
ID Q18667
AC Q18667;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE C47D12.1 protein.
GN C47D12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea.
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gajadary S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for investigating biology."
RT Science 282:2012-2018(1998).
RL EMBL; 269902; CAA93765.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR003151; FAT.
DR InterPro: IPR003152; FAT.
DR InterPro: IPR00403; P13_P14_kinase.
DR Pfam: PF02259; FAT; 1.
DR Pfam: PF02260; FATC; 1.
DR Pfam: PF00454; P13_P14_kinase; 1.
DR SMART; SM00146; P13Kc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN.1.
SQ SEQUENCE 3944 AA; 452752 MW; AD1B1971F16D923 CRC64;
Query Match 95.5%; Score 42; DB 5; Length 3944;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLYWIP 6
GN 111111
DB 3252 WLYWIP 3257

RESULT 2

Q9D029 PRELIMINARY: PRT: 309 AA.
AC Q9D029:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE DNA segment, Chr 7, Wayne state University 128, expressed (Unknown)
DE (Protein for MGC:19443).
GN D7WSU128.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]

SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRIO;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whiteaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[2]

RA SEQUENCE FROM N.A.
RA Strausberg R.;
RI Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RI EMBL: AK011862; BAB2786.1; -;
RI EMBL: BC011313; AAH11313.1; -;
RI MGD: MGI:107301; D7WSU128.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00213; UBO; 1.
DR PROSITE: PS00299; UBIQUITIN_1; UNKNOWN_1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 309 AA; 33449 MW; 9063FACBAE5A9C8E CRC64;

Query Match 90.9%; Score 40; DB 11; Length 309;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLYWIP 6
GN 111111
DB 286 WLYWIP 291

RESULT 3
O14562 PRELIMINARY: PRT: 533 AA.
AC O14562:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gene product with similarity to ubiquitin binding enzyme.
GN A-73566.2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.D., Kim U.T., Sneddon V.P., Kalush F., Brandon R.,
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S.,
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from
human chromosome 16p and 16q."
RL Genomics 60:285-308(1999).
DR EMBL: AC002400; AAC05812.1; -;
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00213; UBO; 1.
DR PROSITE: PS00299; UBIQUITIN_1; UNKNOWN_1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 533 AA; 56895 MW; 500B38770EC03595 CRC64;

Query Match 90.9%; Score 40; DB 4; Length 533;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLYWIP 6
GN 111111
DB 510 WLYWIP 515

RESULT 4
Q9XW49 PRELIMINARY: PRT: 1564 AA.
AC Q9XW49:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Y53C10A.9 protein.
GN Y53C10A.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxId=6239;
[1]

RP SEQUENCE FROM N.A.
RP White S.;
RI Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
RI [2]
RA SEQUENCE FROM N.A.
RX MEDLINE=99063613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: AL033536; CA22142.1; -;
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001623; ABC_tran; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR Prodom: PD000006; ABC_transporter; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_2.
DR PROSITE: PS00636; DNAJ_1; UNKNOWN_1.
SQ SEQUENCE 1564 AA; 176701 MW; DC66A37ED8DC50F CRC64;

Query Match 88.6%; Score 39; DB 5; Length 1564;
Best Local Similarity 66.7%; Pred. No. 3,3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLYWIP 6
GN 111111

Db 326 WLFWP 331

RESULT 5
08XZ08 PRELIMINARY: PRT: 71 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Putative transmembrane protein.
GN RSC1297 OR R502819.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brothier P., Camu J.C., Catolico L.,
Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
Siglier P., Thebaud P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
RA Genome sequence of the plant pathogen Ralstonia solanacearum.;
RT Nature 415:497-502(2002).
RL EMBL: AL646063; CADI4999.1; -.
KW Complete proteome.
SQ SEQUENCE 71 AA; 8263 MW; F10632B9CF260C49 CRC64;

Query Match 86.4%; Score 38; DB 16; Length 71;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLFWP 6
|:|:|
Db 44 WLFWP 49

RESULT 6
09V596 PRELIMINARY: PRT: 142 AA.

AC 09V596;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE CG12929 protein.
GN CG12929.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gelinkler S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champs M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
Abril J.F., Abmayy A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Balew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Moharry C., Morris J., Mostrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA The genome sequence of Drosophila melanogaster.;
RT Science 287:2185-2195(2000).
RL EMBL: AE003833; AAF58921.1; -.
DR Flybase: FBgn0033429; CG12929.
SQ SEQUENCE 142 AA; 15642 MW; 20DEA503BDC12DB CRC64;

Query Match 86.4%; Score 38; DB 5; Length 142;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLFWP 6
|:|:|:|
Db 53 WLFWP 58

RESULT 7
09I118 PRELIMINARY: PRT: 211 AA.

AC 09I118;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, last annotation update)
DE Hypothetical protein PA2287.
GN PA2287.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagron M.,
Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yan Y.,
Smith L.L., Coulter S.N., Folger K.R., Kas A., Larij K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RT Nature 406:959-964(2000).
RL EMBL: AE004654; AAG05673.1; -.
DR EMBL: AE004654; AAG05673.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 211 AA; 23043 MW; 201B4710FE84AB59 CRC64;

Query Match 86.4%; Score 38; DB 16; Length 211;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLFWP 6
|:|:|:|

Db 59 WLFMLP 64

RESULT 8

Q21056 PRELIMINARY: PRT; 402 AA.
AC Q21056;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Fatty acid desaturase.
GN FAT.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Spychalla J.P., Browse J.;
"The fat-1 gene of Caenorhabditis elegans encodes an omega-3 fatty acid desaturase".
KL Submitted (Mar-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: L41807; AAA67369.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR Prodom: PDD001081; FA_desaturase; 2.
SQ SEQUENCE 402 AA; 46545 MW; A26ADAC6F05B0F0 CRC64;

Query Match 86.4%; Score 38; DB 5; Length 402;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
1 11:1
Db 261 WYWVP 266

RESULT 9

Q9NE00 PRELIMINARY: PRT; 402 AA.
AC Q9NE00;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Y67H2A a protein (Y67H2A.8 protein).
GN Y67H2A.A OR Y67H2A.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sulston J.E.;
Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for investigating biology".
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Sulston J.E.;
Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL132901; CAB60965.1; -.
DR EMBL: AL132951; CAC44309.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR Prodom: PDD001081; FA_desaturase; 2.
SQ SEQUENCE 402 AA; 46559 MW; BEIBICD794EA98C5 CRC64;

Query Match 86.4%; Score 38; DB 5; Length 402;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
1 11:1
Db 261 WYWVP 266

RESULT 10

O96T23 PRELIMINARY: PRT; 564 AA.
AC O96T23;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 62.9 kDa protein.
GN B9B15.005.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Allyn V., Hobeisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (Dec-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
Submitted (Nov-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1 SIMILARITY: CONTAINS 1 FUNGAL-TYPE BINUCLEAR CLUSTER DOMAIN.
DR EMBL: AL451014; CAD11346.1; -.
DR InterPro: IPR001138; Fungl_TRN.
DR Pfam: PF001172; Zn_Clus; 1.
DR PROSITE: PS00463; ZN2_CY6_FUNGAL_1; UNKNOWN_1.
DR PROSITE: PS50048; ZN2_CY6_FUNGAL_2; 1.
KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW Transcription regulation; Zinc.
SQ SEQUENCE 564 AA; 62860 MW; A7054767236C3CB CRC64;

Query Match 86.4%; Score 38; DB 3; Length 564;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLYWIP 6
1 11:1
Db 329 WLFMLP 334

RESULT 11

O01260 PRELIMINARY: PRT; 739 AA.
AC O01260;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T20D3.11 protein.
GN T20D3.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
Submitted (Dec-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for investigating biology".
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Sulston J.E.;
Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL132901; CAB60965.1; -.
DR EMBL: AL132951; CAC44309.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR Prodom: PDD001081; FA_desaturase; 2.
SQ SEQUENCE 402 AA; 46559 MW; BEIBICD794EA98C5 CRC64;

RL Science 282:2012-2018(1998).
DR EMBL: Z68220; CAA92491.1; -
SQ SEQUENCE 739 AA; 85116 MW; 47363290D1510329 CRC64;

Query Match 86.4%; Score 38; DB 5; Length 739;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
| | | | |
Db 475 WSWYWP 480

RESULT 12
098GK3

ID 098GK3 PRELIMINARY; PRT; 739 AA.

AC 098GK3:
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
Hypothetical protein ml13287.
ML3287.

OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;

RX Kaneo T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
Watanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto A., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL: AP003001; BAB50213.1; -
DR InterPro: IPR001880; MSion_channel.

DR Pfam: PF00924; MS_channel; 1.
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 739 AA; 81423 MW; E57C8EB5A704087 CRC64;

Query Match 86.4%; Score 38; DB 16; Length 739;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 WLYWIP 6
| | | | |
Db 259 WFWYWP 264

RESULT 13
064622

ID 064622 PRELIMINARY; PRT; 68 AA.

AC 064622:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein-tyrosine-phosphatase (EC 3.1.3.48) (Fragment).
PTP-S.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
MEDLINE=96125184; PubMed=8534367;

RX Reddy R.S., Swatup G.;

RT "Alternative splicing generates four different forms of a non-
transmembrane protein tyrosine phosphatase mRNA.";

RL DNA Cell Biol. 14:1007-1015(1995).

DR EMBL: X92747; CAA63406.1; -

DR Hydrolase.

FT NON_TER

SQ SEQUENCE 68 AA; 8194 MW; DA5293915CABCBF CRC64;

Query Match 84.1%; Score 37; DB 11; Length 68;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
| | | | |
Db 35 WLYWQP 40

RESULT 14
091BA4

ID 091BA4 PRELIMINARY; PRT; 322 AA.

AC 091BA4:
DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE RYTPN3 protein (Fragment).

GN RYTPN3.

OS Potamotrygon motoro (South American freshwater stingray).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hypnosquales; Pristiogaster; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.

OX NCBI_TaxID=86373;
[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20219325; PubMed=10754074;

RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
vertebrates.";

RL J. Mol. Evol. 50:302-311(2000).

DR EMBL: AB033582; BAA95189.1; -
DR HSSP: P18031; 1BXJ

DR InterPro: IPR000387; TYR_phosphatase.

DR InterPro: IPR000242; TYR_PP.

DR Pfam: PF00102; Y_phosphatase; 1.

DR PRINTS: PR00700; PRTYHPHTASE.

DR SMART: SM00194; PTPC; 1.

DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.

DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.

KW Hydrolase.

FT NON_TER

SQ SEQUENCE 322 AA; 36954 MW; B0045D23E66F1197 CRC64;

Query Match 84.1%; Score 37; DB 13; Length 322;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 WLYWIP 6
| | | | |
Db 293 WLYWKP 298

RESULT 15
099M14

ID 099M14 PRELIMINARY; PRT; 340 AA.

AC 099M14:
DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Cathepsin S.

GN CTSS.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002125; AH02125.1; -.
 DR HSSP; P25774; IBEF.
 DR MEROPS; C01.034; -.
 DR MGD; MGI:107341; Ctss.
 DR InterPro; IPR000668; Peptidase_C1.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPA1N.
 DR PRODOM; PD000158; Peptidase_C1; 1.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hydrolase; Thiol protease.
 SQ SEQUENCE 340 AA; 38456 MW; 076502611F319DB7 CRC64;

Query Match 84.1%; Score 37; DB 11; Length 340;
 Fast Local Similarity 66.7%; Pred No. 1.7e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLYWIP 6
 ||:|:|
 DB 11 WLFWMP 16

Search completed: January 3, 2003, 15:31:58
 Job time : 22.3182 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:16 ; Search time 9 seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-543-188A-4

Perfect score: 44

Sequence: 1 WLWIP 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

al number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PC10S.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	86.4	402	4	US-09-025-578-2
2	38	86.4	402	4	US-09-330-235-2
3	34	77.3	10	2	US-08-556-597-159
4	34	77.3	17	1	US-08-190-788A-233
5	34	77.3	17	1	US-08-383-474B-236
6	34	77.3	17	1	US-08-465-391A-233
7	34	77.3	17	2	US-08-464-538B-233
8	34	77.3	17	2	US-08-463-076E-287
9	34	77.3	257	4	US-09-372-422A-28
10	34	77.3	272	4	US-09-372-422A-26
11	34	77.3	511	4	US-08-991-677-4
12	34	77.3	823	1	US-07-745-206A-15
13	34	77.3	823	2	US-08-311-363-15
14	34	77.3	1754	1	US-07-745-206A-13
15	34	77.3	1754	1	US-08-311-363-13
16	34	77.3	2237	1	US-08-455-543A-48
17	34	77.3	2237	1	US-08-223-305C-48
18	34	77.3	2237	4	US-09-268-163-8
19	34	77.3	2265	4	US-08-149-097D-36
20	34	77.3	2336	4	US-09-268-163-10
21	34	77.3	2337	4	US-08-713-118-2
22	34	77.3	2337	4	US-09-452-007-2
23	34	77.3	2339	1	US-08-455-543A-47
24	34	77.3	2339	2	US-08-223-305C-47
25	34	77.3	2339	4	US-09-268-163-6
26	34	77.3	2343	4	US-09-268-163-4
27	34	77.3	2509	2	US-08-149-097D-35

28	33	75.0	118	4	US-09-134-001C-4174	Sequence 4174, Ap
29	33	75.0	134	4	US-09-273-163-8	Sequence 8, Appl
30	33	75.0	247	4	US-09-372-422A-48	Sequence 48, Appl
31	33	75.0	249	4	US-09-372-422A-22	Sequence 22, Appl
32	33	75.0	249	4	US-09-372-422A-30	Sequence 30, Appl
33	33	75.0	249	4	US-09-372-422A-6	Sequence 6, Appl
34	33	75.0	250	4	US-09-372-422A-24	Sequence 24, Appl
35	33	75.0	254	4	US-09-372-422A-34	Sequence 34, Appl
36	33	75.0	576	4	US-08-864-785-1	Sequence 1, Appl
37	33	75.0	608	4	US-09-134-001C-3395	Sequence 3395, Ap
38	33	75.0	674	1	US-08-803-973-7	Sequence 7, Appl
39	33	75.0	674	1	US-08-803-973-7	Sequence 7, Appl
40	33	75.0	707	1	US-08-803-973-12	Sequence 12, Appl
41	33	75.0	707	1	US-08-803-973-12	Sequence 12, Appl
42	33	75.0	746	1	US-08-476-519-11	Sequence 11, Appl
43	33	75.0	746	5	PCT-US95-09323-11	Sequence 11, Appl
44	33	75.0	777	1	US-08-476-519-2	Sequence 2, Appl
45	33	75.0	777	5	PCT-US95-09323-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-025-578-2
; Sequence 2, Application US/09025578
; Patent No. 6194167
; GENERAL INFORMATION:
; APPLICANT: John A. Browne and James P. Spychalla
; TITLE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan E. Dow, Ph.D.
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,578
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/038,409
; FILING DATE: February 18, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan E. Dow, Ph.D.
; REGISTRATION NUMBER: 35,123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; US-09-025-578-2
; Query Match 86.4%; Score 38; DB 4; Length 402;
; Best Local Similarity 66.7%; Pred. No. 65;
; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
; QY 1 WLWIP 6

Db 261 WYMWVP 266

RESULT 2
US-09-330-235-2
Sequence 2, Application US/09330235
Patent No. 6459018
GENERAL INFORMATION:
APPLICANT: Knutson, Debbie
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
FILE REFERENCE: MOCO.156.000S
CURRENT APPLICATION NUMBER: US/09/330,235
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 402
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-330-235-2

Query Match 86.4%; Score 38; DB 4; Length 402;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 WLMWP 6
1 1 1 1
Db 261 WYMWVP 266

RESULT 3
US-08-556-597-159
Sequence 159, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN ID/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devens & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid.

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-159

Query Match 77.3%; Score 34; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.8;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMWP 6
1 1 1 1
Db 3 WLMHWP 8

RESULT 4
US-08-190-788A-233
Sequence 233, Application US/08190788A
Patent No. 5608035
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies N.V.
STREET: 4001 Miranda Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,788A
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 233:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-190-788A-233

Query Match 77.3%; Score 34; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLMWP 6
1 1 1 1
Db 4 WYMWVP 9

RESULT 5
US-08-383-474B-236
Sequence 236, Application US/08383474B

Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-474B-236

Query Match 77.3%; Score 34; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 WLXWIP 6
|:|:|:|
DB 4 WYVWOP 9

RESULT 6
US-08-465-391A-233
Sequence 233, Application US/08465391A
Patent No. 5766331
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Boyy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottoft, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331v1e1, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 233:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-233

Query Match 77.3%; Score 34; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLXWIP 6
|:|:|:|
DB 4 WYVWOP 9

RESULT 7
US-08-464-538B-233
Sequence 233, Application US/08464538B
Patent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Boyy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottoft, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 233:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-233

Query Match 77.3%; Score 34; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLXWIP 6
|:|:|
Db 4 WYVWQP 9

RESULT 8
US-08-463-076E-287
Sequence 287, Application US/08463076E
Patent No. 5880096
GENERAL INFORMATION:
APPLICANT: Barlett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001800S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 287:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid.

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-287

Query Match 77.3%; Score 34; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLXWIP 6
|:|:|
Db 4 WYVWQP 9

RESULT 9
US-09-372-422A-28
Sequence 28, Application US/09372422A
Patent No. 6313375
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Barlieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 257
TYPE: PRT
ORGANISM: Zea mays
US-09-372-422A-28

Query Match 77.3%; Score 34; DB 4; Length 257;
Best Local Similarity 80.0%; Pred. No. 1,7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWI 5
|:|:|
Db 222 WYVWI 226

RESULT 10
US-09-372-422A-26
Sequence 26, Application US/09372422A
Patent No. 6313375
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Barlieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 272
TYPE: PRT
ORGANISM: Zea mays
US-09-372-422A-26

Query Match 77.3%; Score 34; DB 4; Length 272;
Best Local Similarity 80.0%; Pred. No. 1,8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWI 5
|:|:|
Db 220 WYVWI 224

RESULT 11
US-08-991-677-4
; Sequence 4, Application US/08991677A
; Patent No. 6252135
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Carraway, Daniel T
; APPLICANT: Smeltzer, Richard H
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
; FILE REFERENCE: 50617
; CURRENT APPLICATION NUMBER: US/08/991,677A
; CURRENT FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: US 60/033,381
; EARLIER FILING DATE: 1996-12-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
; US-08-991-677-4

Query Match 77.3%; Score 34; DB 4; Length 511;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLXWIP 6
|||:|
Db 224 WLKWP 229

RESULT 12
US-07-745-206A-15
; Sequence 15, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745,206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 823 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-745-206A-15

Query Match 77.3%; Score 34; DB 1; Length 823;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWIP 6
|||:|
Db 333 WLXWIP 338

RESULT 13
US-08-311-363-15
; Sequence 15, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 823 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-311-363-15

Query Match 77.3%; Score 34; DB 2; Length 823;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWIP 6
|||:|
Db 333 WLXWIP 338

RESULT 14
US-07-745-206A-13
; Sequence 13, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Filch, Even, Tablin & Flannery
STREET: 135 S. Lasalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ. ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-206A-13

Query Match 77.3%; Score 34; DB 1; Length 1754;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWIP 6
111:11
DB 333 WLXWIP 338

RESULT 15
US-08-311-363-13
Sequence 13, Application US/08311363
Patent No. 5876958
GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311.363
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ. ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-13

Query Match 77.3%; Score 34; DB 2; Length 1754;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWIP 6
111:11
DB 333 WLXWIP 338

Search completed: January 3, 2003, 15:34:28
Job time: 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:32:11 ; Search time 4.77273 Seconds
(without alignments)
23.825 Million cell updates/sec

Title: US-09-543-188A-4
Perfect score: 44
Sequence: 1 WLWIP 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues
al number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PC1US_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	86.4	402	9	US-10-104-339-2
2	38	86.4	402	10	US-09-747-755-2
3	36	81.8	456	10	US-09-801-368-204
4	35	79.5	83	10	US-09-864-761-47931
5	35	79.5	360	10	US-09-815-242-11186
6	35	79.5	475	10	US-09-815-242-10052
7	34	77.3	446	9	US-10-042-141-58
8	34	77.3	446	10	US-09-726-643-58
9	34	77.3	510	9	US-10-042-141-139
10	34	77.3	510	10	US-09-726-643-139
11	34	77.3	511	10	US-09-796-256A-4
12	34	77.3	627	10	US-09-862-027-46
13	34	77.3	1034	9	US-09-738-626-4785
14	34	77.3	1189	9	US-09-738-626-4140
15	34	77.3	2237	12	US-10-033-026-8
16	34	77.3	2336	12	US-10-033-026-10
17	34	77.3	2339	12	US-10-033-026-6
18	34	77.3	2343	12	US-10-033-026-4
19	33	75.0	31	9	US-10-016-157A-201

20	33	75.0	56	10	US-09-864-761-35892	Sequence 35892, A
21	33	75.0	88	10	US-09-764-853-591	Sequence 591, App
22	33	75.0	126	10	US-09-864-761-48848	Sequence 48848, A
23	33	75.0	221	10	US-09-925-300-1659	Sequence 1659, App
24	33	75.0	235	10	US-09-864-711-15	Sequence 15, App1
25	33	75.0	262	9	US-09-981-353-63	Sequence 63, App1
26	33	75.0	288	10	US-09-925-299-840	Sequence 840, App
27	33	75.0	365	10	US-09-815-242-13185	Sequence 13185, A
28	33	75.0	398	10	US-09-729-674-146	Sequence 146, App
29	33	75.0	463	9	US-09-738-626-6546	Sequence 6946, App
30	33	75.0	466	10	US-09-815-242-10265	Sequence 10265, A
31	33	75.0	466	10	US-09-815-242-14048	Sequence 14048, A
32	33	75.0	475	10	US-09-815-242-5055	Sequence 5055, App
33	33	75.0	475	10	US-09-815-242-11503	Sequence 11503, A
34	33	75.0	519	9	US-09-895-913A-118	Sequence 118, App
35	33	75.0	519	10	US-09-815-242-11388	Sequence 11388, A
36	33	75.0	559	10	US-09-820-721A-1	Sequence 1, App1
37	33	75.0	563	10	US-09-915-181A-6	Sequence 6, App1
38	33	75.0	777	10	US-09-815-242-4894	Sequence 4894, App
39	33	75.0	914	10	US-09-815-242-10897	Sequence 10897, A
40	33	75.0	1167	10	US-09-815-242-11522	Sequence 11522, A
41	32	72.7	70	10	US-09-864-761-46021	Sequence 46021, A
42	32	72.7	79	9	US-09-738-626-4898	Sequence 4898, App
43	32	72.7	110	10	US-09-867-550-298	Sequence 298, App
44	32	72.7	116	10	US-09-741-843-4	Sequence 4, App1
45	32	72.7	169	10	US-09-925-301-902	Sequence 902, App

ALIGNMENTS

RESULT 1:
US-10-104-339-2
; Sequence 2, Application US/10104339
; Patent No. US200201/0090A1
GENERAL INFORMATION:
APPLICANT: John A. Browne and James P. Spychalla
TITLE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESS: Alan E. Dow, Ph.D.
STREET: One World Trade Center
Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,339
FILING DATE: 21-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/747,755
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Alan E. Dow, Ph.D.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-4946/AED
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid residues
TYPE: amino acid
STRANDEDNESS: single stranded
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-104-339-2

Query Match 86.4%: Score 38; DB 9; Length 402;
Best Local Similarity 66.7%: Pred. No. 39;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
| | | |
DB 261 WYWWP 266

RESULT 2
US-09-747-755-2

Sequence 2, Application US/09747755
Patent No. US20020042933A1
GENERAL INFORMATION:
APPLICANT: John A. Browse and James P. Spychalla
TITLE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alan E. Dow, Ph.D.
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/747,755

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/025,578

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Alan E. Dow, Ph.D.

REGISTRATION NUMBER: 35,123

REFERENCE/DOCKET NUMBER: 4630-49462/AED

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 226-9446

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 402 amino acid residues

TYPE: amino acid

STRANDEDNESS: single stranded

TOPOLOGY: linear

US-09-747-755-2

Query Match 86.4%: Score 38; DB 10; Length 402;
Best Local Similarity 66.7%: Pred. No. 39;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
| | | |
DB 261 WYWWP 266

RESULT 3
US-09-801-368-204

Sequence 204, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian

APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 204
LENGTH: 456
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-204

Query Match 81.8%: Score 36; DB 10; Length 456;
Best Local Similarity 66.7%: Pred. No. 86;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLYWIP 6
| | | |
DB 22 WYWWP 27

RESULT 4
US-09-864-761-47931

Sequence 47931, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47931
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009402.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EST_HUMAN HIT: BF090287.1, EVALU6 3.10e-01
; OTHER INFORMATION: SWISSPROT HIT: P13276, EVALU6 1.90e+00
; US-09-864-761-47931

Query Match
Best Local Similarity 79.5%; Score 35; DB 10; Length 83;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWI 5
Db 17 WLXWL 21

RESULT 5
US-09-815-242-11186
; Sequence 1186, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11186
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
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US-09-815-242-11186

Query Match
Best Local Similarity 79.5%; Score 35; DB 10; Length 360;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWI 5
Db 147 WLXWL 151

RESULT 6
US-09-815-242-10052
; Sequence 10052, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10052
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-815-242-10052

Query Match
Best Local Similarity 79.5%; Score 35; DB 10; Length 475;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLXWI 5
Db 105 WLXWL 109

RESULT 7
US-10-042-141-58
; Sequence 58, Application US/10042141
; Publication No. US20020183503A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/10/042,141
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/726,643
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
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PRIORITY FILING DATE: 2000-06-02
PRIORITY FILING DATE: 2000-06-02
PRIORITY APPLICATION NUMBER: 60/137,725
PRIORITY FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: Patentl Ver. 2.0
SEQ ID NO 58
LENGTH: 446
TYPE: PRt
ORGANISM: Homo sapiens
US-10-042-141-58

```

Query Match	77.38;	Score 34;	DB 9;	Length 446;
Best Local Similarity	80.0%;	Pred. No. 1.7e+02;		
Matches	4;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	WLYWI	5
		:	
Db	141	WVYWI	145

09-09-726-643-58
JLT 8

Sequence 58, Application of US/09726643
Patent No. US2002008449A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: P2040P1
CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
US-09-726-643-58

Query Match	77.38;	Score 34;	DB 10;	Length 446;
Best Local Similarity	80.08;	Pred. No. 1.7e+02;		
Matches	4;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	WLYWI	5
		1:111	
	141	WVYWI	145

RESULT 9
US-10-042-141-139

Sequence 139, Application US/10042141
Publication No. US20020183503A1
GENERAL INFORMATION:

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; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/10/042,141

```

;; PRIOR APPLICATION NUMBER: 09/726,643
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US00/15187

```

: PRIOR APPLICATION NUMBER: 60/137,725
:
: PRIOR FILING DATE: 1999-06-07
:
: NUMBER OF SEQ ID NOS: 190

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 510
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TYPE: PRT
ORGANISM: Homo sapiens

US-10-042-141-139

Query Match	77.38;	Score 34;	DB 9;	Length 510;
Best Local Similarity	80.08;	Pred. No. 1.9e+02;		
Matches	4;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

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QY      1 WLXWI 5
        | : |||
Db      205 WYXWI 209
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RESULT 10
US-09-726-643-139

Sequence 139, Application US/09726643
Patent No. US20020028449A1

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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P204001

```

; CURRENT APPLICATION NUMBER: US/09/726,643
 ;
 ; CURRENT FILING DATE: 2000-12-01
 ;
 ; PRIOR APPLICATION NUMBER: PCT/US00/15187
 ;
 ; PRIOR FILING DATE: 2000-06-02

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; PRIOR APPLICATION NUMBER: 60/137,725
;
; PRIOR FILING DATE: 1999-06-07
;
; NUMBER OF SEQ ID NOS: 190
;
; SOFTWARE: PatentIn Ver. 2.0

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```
; SEQ ID NO 139
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
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```
US-09-726-643-139
Query Match      77.3%; Score 34; DB 10; Length 510;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
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Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	WLWWT	5						
		I : I I I							
db	205	WVYWI	209						

RESULT 11
US-09-796-256A-4
; Sequence 4, Application US/09796256A
; Patent No. US20020078477A1

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; GENERAL INFORMATION:
;
; APPLICANT: Chiang, Vincent L
; APPLICANT: Carraway, Daniel T
; APPLICANT: Smeltzer, Richard H

```

```

; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
;
; FILE REFERENCE: 50617/c-3532.0
;
; CURRENT APPLICATION NUMBER: US/09/796,256A
;
; CURRENT FILING DATE: 2001-02-28

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PRIOR APPLICATION NUMBER: US60/033381
PRIOR FILING DATE: 1996-12-16
PRIOR APPLICATION NUMBER: 08/991677
PRIOR FILING DATE: 1997-12-12

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: NUMBER OF SEQ ID NOS: 11
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: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO 4
:
: LENGTH: 511
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; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
US-09-796-256A-4

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Query Match 77.3%; Score 34; DB 10; Length 511;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Indels 0; Gaps 0;

QY	1	WLWIP	6
	11	11	1
Db	224	WLKWP	229

RESULT 12
US-09-862-027-46
; Sequence 46, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:
; APPLICANT: HODGE, Martin R.
; TITLE OF INVENTION: NO. US20020142428A1 Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Mus musculus
09-862-027-46

Query Match 77.3%; Score 34; DB 10; Length 627;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WLYWIP 6
|||:|
Db 210 WLMWAP 215

RESULT 13
US-09-738-626-4785
; Sequence 4785, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4785
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4785

Query Match 77.3%; Score 34; DB 9; Length 1034;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYWIP 5
|||:|
Db 563 WLYWM 567

RESULT 14
US-09-738-626-4140
; Sequence 4140, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4140
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4140

Query Match 77.3%; Score 34; DB 9; Length 1189;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WLYWIP 6
|||:|
Db 247 WLMWAP 252

RESULT 15
US-10-033-026-8
; Sequence 8, Application US/10033026
; Patent No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B105577000
; CURRENT APPLICATION NUMBER: US/10/033,026
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-026-8

Query Match 77.3%; Score 34; DB 12; Length 2237;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYWIP 6
|||:|
Db 333 WLYEIP 338

Mon Jan 6 15:09:04 2003

us-09-543-188a-4.rapb

Page 6

Search completed: January 3, 2003, 15:52:05
Job time : 5.77273 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:16 : Search time 9 seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-543-188a-13

Perfect score: 24

Sequence: 1 LLLVIA 6

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Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	100.0	112	1	US-07-800-364B-15
2	24	100.0	173	4	US-09-134-001C-4275
3	24	100.0	509	3	US-08-688-988-40
4	24	100.0	630	4	US-09-134-001C-4615
5	23	95.8	387	4	US-09-134-001C-4298
6	23	95.8	503	4	US-08-740-223A-18
7	23	95.8	503	4	US-09-134-001C-3948
8	23	95.8	503	4	US-09-202-491-4
9	23	95.8	503	4	US-09-202-491-10
10	23	95.8	503	4	US-09-709-188-18
11	23	95.8	913	1	US-08-445-640-4
12	23	95.8	913	3	US-08-170-558-4
13	23	95.8	913	3	US-08-447-314-4
14	23	95.8	913	3	US-08-445-461-4
15	23	95.8	919	3	US-08-336-343A-2
16	23	95.8	1210	2	US-08-484-438-7
17	23	95.8	1210	2	US-08-475-035-4
18	22	91.7	30	4	US-08-448-488-7
19	22	91.7	88	1	US-08-091-569-21
20	22	91.7	88	1	US-08-203-676-21
21	22	91.7	88	2	US-08-822-238-21
22	22	91.7	126	4	US-09-288-143-71
23	22	91.7	128	6	5179198-1
24	22	91.7	128	6	5521296-1
25	22	91.7	177	3	US-08-465-794-17
26	22	91.7	177	3	US-09-049-813-17
27	22	91.7	295	4	US-08-937-067-2

28	22	91.7	323	6	5185254-4	Patent No. 5185254
29	22	91.7	344	2	US-08-475-634D-19	Sequence 19, Appl
30	22	91.7	353	4	US-09-134-001C-4325	Sequence 4325, Ap
31	22	91.7	359	1	US-07-662-005A-4	Sequence 4, Appl
32	22	91.7	503	4	US-09-382-256-10	Sequence 10, Appl
33	22	91.7	503	4	US-09-395-115-10	Sequence 10, Appl
34	22	91.7	503	4	US-08-436-265-10	Sequence 10, Appl
35	22	91.7	503	4	US-09-679-187-10	Sequence 10, Appl
36	22	91.7	514	4	US-09-717-432-2	Sequence 2, Appl
37	22	91.7	514	4	US-09-912-484-2	Sequence 2, Appl
38	22	91.7	579	3	US-08-704-711A-1	Sequence 1, Appl
39	22	91.7	579	4	US-09-521-220-1	Sequence 1, Appl
40	22	91.7	582	3	US-08-704-711A-2	Sequence 2, Appl
41	22	91.7	582	4	US-08-448-489-1	Sequence 1, Appl
42	22	91.7	582	4	US-09-211-704A-9	Sequence 9, Appl
43	22	91.7	582	4	US-09-521-220-2	Sequence 2, Appl
44	22	91.7	582	4	US-09-391-104-28	Sequence 28, Appl
45	22	91.7	976	2	US-08-449-645A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-07-800-364B-15
; Sequence 15, Application US/07800364B
; Patent No. 5688678
; GENERAL INFORMATION:
; APPLICANT: Hewick, Rodney M.
; APPLICANT: Wang, Jack H.
; APPLICANT: Mooney, John M.
; APPLICANT: Celeste, Anthony J.
; TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/800,364B
; FILING DATE: 26-NOV-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5182A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-07-800-364B-15
Query Match 100.0%; Score 24; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLVIA 6

Db 26 LLLVIA 31
|||||

RESULT 2
US-09-134-001C-4275

; Sequence 4275, Application US/09134001C
; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/134,001C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4275

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4275

Query Match 100.0%; Score 24; DB 4; Length 173;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
|||||

Db 28 LLLVIA 33

RESULT 3
US-08-688-988-40

; Sequence 40, Application US/08688988B

; Patent No. 6096545

; GENERAL INFORMATION:

; APPLICANT: Lefebvre, Daniel D.

; APPLICANT: Malibochi, Mohammad A.

; TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS

; FILE REFERENCE: PPL96-03

; CURRENT APPLICATION NUMBER: US/08/688,988B

; PRIOR FILING DATE: 1996-07-31

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 40

; LENGTH: 509

; TYPE: PRT

; ORGANISM: Hordeum vulgare

US-08-688-988-40

Query Match 100.0%; Score 24; DB 3; Length 509;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
|||||

Db 7 LLLVIA 12

RESULT 4
US-09-134-001C-4615

; Sequence 4615, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4615

; LENGTH: 630

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4615

Query Match 100.0%; Score 24; DB 4; Length 630;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
|||||

Db 133 LLLVIA 138

RESULT 5
US-09-134-001C-4298

; Sequence 4298, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/134,001C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4298

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4298

Query Match 95.8%; Score 23; DB 4; Length 387;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
|||||

Db 3 LLLVIA 8

RESULT 6
US-08-740-223A-18

; Sequence 18, Application US/08740223A

; Patent No. 6265564

; GENERAL INFORMATION:

; APPLICANT: Davis, et al.

; TITLE OF INVENTION: Expressed ligand - Vascular

; NUMBER OF SEQUENCES: 28
Intercellular Signalling Molecule

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Regeneron Pharmaceuticals, Inc.

; STREET: 777 Old Saw Mill Road

; CITY: Tarrytown

; STATE: NY

; COUNTRY: USA

; ZIP: 10591

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: TIE ligand-4
LOCATION: 1...503
OTHER INFORMATION:
US-08-740-223A-18

Query Match 95.8%; Score 23; DB 4; Length 503;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
Db 12 LLLVIA 17

RESULT 7
US-09-134-001C-3948
Sequence 3948, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3948
LENGTH: 503
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3948

Query Match 95.8%; Score 23; DB 4; Length 503;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
Db 268 LLLVIA 273

RESULT 8
US-09-202-491-4
Sequence 4, Application US/09202491
Patent No. 6432667
GENERAL INFORMATION:
FILE REFERENCE: REG 333-2

APPLICANT: Valenzuela et al.
TITLE OF INVENTION: NOVEL LIGANDS, METHODS OF MAKING AND USES THEREOF
FILE REFERENCE: REG330-K
CURRENT APPLICATION NUMBER: US/09/202,491
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: PCT/US97/10728
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER FILING DATE: 1996-08-02
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER FILING DATE: 1996-07-02
EARLIER APPLICATION NUMBER: 08/665,926
EARLIER FILING DATE: 1996-06-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 503
TYPE: PRT
ORGANISM: Homo sapiens
US-09-202-491-4

Query Match 95.8%; Score 23; DB 4; Length 503;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
Db 12 LLLVIA 17

RESULT 9
US-09-202-491-10
Sequence 10, Application US/09202491
Patent No. 6432667
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: NOVEL LIGANDS, METHODS OF MAKING AND USES THEREOF
FILE REFERENCE: REG330-K
CURRENT APPLICATION NUMBER: US/09/202,491
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: PCT/US97/10728
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER FILING DATE: 1996-08-02
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER FILING DATE: 1996-07-02
EARLIER APPLICATION NUMBER: 08/665,926
EARLIER FILING DATE: 1996-06-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 503
TYPE: PRT
ORGANISM: Homo sapiens
US-09-202-491-10

Query Match 95.8%; Score 23; DB 4; Length 503;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
Db 12 LLLVIA 17

RESULT 10
US-09-709-188-18
Sequence 18, Application US/09709188
Patent No. 6441137
GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
FILE REFERENCE: REG 333-2

;; CURRENT APPLICATION NUMBER: US/09/709,188
;; CURRENT FILING DATE: 2000-11-09
;; PRIOR APPLICATION NUMBER: 08/740,223
;; PRIOR FILING DATE: 1996-10-25
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: Patent version 3.1
;; SEQ ID NO: 18
;; LENGTH: 503
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-709-188-18

Query Match 95.8%; Score 23; DB 4; Length 503;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
DB 12 LLLVIA 17

RESULT 11
US-08-445-640-4
; Sequence 4, Application US/08445640
; Patent No. 5709858
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Scadden, David T.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Barton, Will F.
; TITLE OF INVENTION: Protein Tyrosine Kinases
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,640
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/170558
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/157563
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 854C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-445-640-4

Query Match 95.8%; Score 23; DB 1; Length 913;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
DB 430 LLLVIA 435

RESULT 12
US-08-170-558-4
; Sequence 4, Application US/08170558
; Patent No. 6001621
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Scadden, David T.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Barton, Will F.
; TITLE OF INVENTION: Protein Tyrosine Kinases
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,558
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/157563
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 854C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-170-558-4

Query Match 95.8%; Score 23; DB 3; Length 913;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
DB 430 LLLVIA 435

RESULT 13
US-08-447-314-4
; Sequence 4, Application US/08447314
; Patent No. 6087144
; GENERAL INFORMATION:
; APPLICANT: Scadden, David T.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Barton, Will F.
; TITLE OF INVENTION: Protein Tyrosine Kinases
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,314
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854C1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-447-314-4
Query Match
Best Local Similarity 83.3%; Score 23; DB 3; Length 913;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLLVIA 6
DB 430 LLLVIA 435
RESULT 14
US-08-445-461-4
Sequence 4, Application US/08445461
Patent No. 6096527
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,461
FILING DATE: 22-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-445-461-4
Query Match
Best Local Similarity 83.3%; Score 23; DB 3; Length 913;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLLVIA 6
DB 430 LLLVIA 435
RESULT 15
US-08-336-343A-2
Sequence 2, Application US/08336343A
Patent No. 5677144
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Alves, Freuke
TITLE OF INVENTION: CCK-2, A No. 5677144e1 Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-336-343A-2
Query Match
Best Local Similarity 83.3%; Score 23; DB 1; Length 919;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLEVIA 6
| | : | |
Db 430 LLEVIA 435

Search completed: January 3, 2003, 15:34:29
Job time : 10 secs

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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:32:11 : Search time 4.77273 Seconds
(without alignments)
23.825 Million cell updates/sec

Title: US-09-543-188a-13

Perfect score: 24
Sequence: 1 LLVIA 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Minimum number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	96	US-10-016-481-11	Sequence 11, App1
2	24	100.0	179	US-09-764-853-847	Sequence 847, App
3	24	100.0	179	US-09-764-853-847	Sequence 296, App
4	24	100.0	478	US-09-764-853-847	Sequence 225, App
5	24	100.0	487	US-09-764-853-847	Sequence 680, App
6	24	100.0	504	US-09-738-626-4035	Sequence 4035, App
7	24	100.0	713	US-09-978-295A-183	Sequence 183, App
8	24	100.0	713	US-09-978-295A-183	Sequence 183, App
9	24	100.0	713	US-09-978-295A-183	Sequence 183, App
10	24	100.0	713	US-09-978-295A-183	Sequence 183, App
11	24	100.0	713	US-09-978-295A-183	Sequence 183, App
12	24	100.0	859	US-09-529-053-70	Sequence 416, App
13	23	95.8	27	US-09-984-245-179	Sequence 179, App
14	23	95.8	47	US-09-864-761-34868	Sequence 34868, App
15	23	95.8	62	US-10-001-870-116	Sequence 110, App
16	23	95.8	100	US-09-950-933A-40	Sequence 40, App1
17	23	95.8	114	US-09-925-299-976	Sequence 976, App
18	23	95.8	292	US-09-886-055-315	Sequence 315, App
19	23	95.8	318	US-09-815-242-10468	Sequence 10468, App

20	23	95.8	326	US-09-888-615-105	Sequence 105, App
21	23	95.8	377	US-10-091-628-2	Sequence 2, App1
22	23	95.8	394	US-09-925-301-1388	Sequence 1388, App
23	23	95.8	513	US-09-738-626-6860	Sequence 6860, App
24	23	95.8	624	US-09-925-297-738	Sequence 738, App
25	23	95.8	913	US-09-223-490-4	Sequence 4, App1
26	23	95.8	1210	US-09-725-433-2	Sequence 2, App1
27	23	91.7	39	US-09-864-761-47820	Sequence 47820, App
28	22	91.7	69	US-09-864-761-37443	Sequence 37443, App
29	22	91.7	106	US-09-738-626-4602	Sequence 4602, App
30	22	91.7	124	US-09-893-737-262	Sequence 262, App
31	22	91.7	167	US-10-003-152-18	Sequence 18, App1
32	22	91.7	258	US-09-965-529-25	Sequence 25, App1
33	22	91.7	271	US-09-738-626-5557	Sequence 5557, App
34	22	91.7	295	US-09-934-483A-1	Sequence 1, App1
35	22	91.7	295	US-09-934-483A-5	Sequence 5, App1
36	22	91.7	301	US-09-836-602-6	Sequence 6, App1
37	22	91.7	316	US-09-836-602-4	Sequence 4, App1
38	22	91.7	318	US-09-886-055-101	Sequence 101, App
39	22	91.7	322	US-09-815-242-11790	Sequence 11790, App
40	22	91.7	324	US-09-912-020-245	Sequence 245, App
41	22	91.7	359	US-09-925-302-591	Sequence 591, App
42	22	91.7	362	US-09-712-363-184	Sequence 184, App
43	22	91.7	373	US-09-836-602-2	Sequence 2, App1
44	22	91.7	381	US-09-738-626-5049	Sequence 5049, App
45	22	91.7	417	US-09-815-242-10165	Sequence 10165, App

ALIGNMENTS

RESULT 1
US-10-016-481-11
Sequence 11, Application US/10016481
Patent No. US20020115610A1
GENERAL INFORMATION:
APPLICANT: Zhou, Qun-Yong
TITLE OF INVENTION: Prokinecin Polypeptides, Related
FILE REFERENCE: P-UC 5016
CURRENT APPLICATION NUMBER: US/10/016,481
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/245,882
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 96
TYPE: PRT
ORGANISM: Bombina variegata
US-10-016-481-11

Query Match
Best Local Similarity 100.0%; Score 24; DB 12; Length 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVIA 6
Db 10 LLVIA 15

RESULT 2
US-09-764-853-847
Sequence 847, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper

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; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatencIn Ver. 2.0
; SEQ ID NO 847
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (178)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-847
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Query Match          100.0%; Score 24; DB 10; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LLLVIA 6
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DB 134 LLLVIA 139
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RESULT 3
US-09-764-898-296
; Sequence 296, Application US/09764898
; Patent No. US2002090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatencIn Ver. 2.0
; SEQ ID NO: 296
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (178)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-296
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Query Match          100.0%; Score 24; DB 10; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LLLVIA 6
    |||||
DB 134 LLLVIA 139
```

```

RESULT 4
US-09-764-898-225
; Sequence 225, Application US/09764898
; Patent No. US2002090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1201
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```

; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatencIn Ver. 2.0
; SEQ ID NO 225
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-898-225
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Query Match          100.0%; Score 24; DB 10; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LLLVIA 6
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DB 125 LLLVIA 130
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RESULT 5
US-09-764-853-680
; Sequence 680, Application US/09764853
; Patent No. US2002090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatencIn Ver. 2.0
; SEQ ID NO: 680
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-680
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Query Match          100.0%; Score 24; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LLLVIA 6
    |||||
DB 134 LLLVIA 139
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RESULT 6
US-09-738-626-4035
; Sequence 4035, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 248-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4035
LENGTH: 504
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4035

Query Match 100.0%; Score 24; DB 9; Length 504;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
DB 490 LLLVIA 495

RESULT 7
US-09-978-295A-183
Sequence 183, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
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PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 24; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 5; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

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DB 454 LLLVIA 459

RESULT 8
US-09-978-697-183
Sequence 183: Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978, 697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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49	PRIOR APPLICATION NUMBER: 60/081195
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56	PRIOR FILING DATE: 1998-04-15
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60	PRIOR FILING DATE: 1998-04-15
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65	PRIOR APPLICATION NUMBER: 60/082568
66	PRIOR FILING DATE: 1998-04-21
67	PRIOR APPLICATION NUMBER: 60/082569
68	PRIOR FILING DATE: 1998-04-21
69	PRIOR APPLICATION NUMBER: 60/082704
70	PRIOR FILING DATE: 1998-04-22
71	PRIOR APPLICATION NUMBER: 60/082804
72	PRIOR FILING DATE: 1998-04-22
73	PRIOR APPLICATION NUMBER: 60/082700

PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082796
PRIOR FILING DATE:	1998-04-23
PRIOR APPLICATION NUMBER:	60/083356
PRIOR FILING DATE:	1998-04-27
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083392
PRIOR FILING DATE:	1998-04-29
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PRIOR FILING DATE:	1998-05-15
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PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085699

Query Match	100.0%;	Score 24;	DB 9;	Length 713;
Best Local Similarity	100.0%;	Pred. No. 5.6e+02;		

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLLVIA 6
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 Db 454 LLLVIA 459

RESULT 9

US-09-978-192A-183
 ; Sequence 183, Application US/09978192A
 ; Patent No. US2002017553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paonl, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC9
 ; CURRENT APPLICATION NUMBER: US/09/978,192A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 100.0%; Score 24; DB 9; Length 713;
 Best Local Similarity 100.0%; Pred. No. 5; e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 454 LLLVTA 459

RESULT 10
 US-09-999-832A-183
 Sequence 183, Application US/0999832A
 Publication No. US20020192706A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
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 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
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 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC63
 CURRENT APPLICATION NUMBER: US/09/999,832A
 CURRENT FILING DATE: 2001-10-24
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Query Match 100.0%; Score 24; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
DB 454 LLLVIA 459

RESULT 11
US-10-052-586-416
Sequence 416; Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
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PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/086392
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;; PRIOR APPLICATION NUMBER: 60/089090
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;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
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;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
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;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 24; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLLVIA 6
Db 454 LLLVIA 459

RESULT 12
US-09-529-063-70
; Sequence 70, Application US/09529063
; Patent No. US20020102542A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, DAICHI
; APPLICANT: SHIBAYAMA, SHIRO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
; FILE REFERENCE: Q58769
; CURRENT APPLICATION NUMBER: US/09/529,063
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/JP98/04514

;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: JP 9-274674
;; PRIOR FILING DATE: 1997-10-07
;; NUMBER OF SEQ ID NOS: 117
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 70
;; LENGTH: 859
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-529-063-70

Query Match 100.0%; Score 24; DB 10; Length 859;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLLVIA 6
Db 506 LLLVIA 511

RESULT 13
US-09-984-245-179
; Sequence 179, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004PI
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
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; PRIOR FILING DATE: 1997-03-21
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; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 179
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-179

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Best Local Similarity 95.8%; Score 23; DB 9; Length 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
Db 7 LLLVIA 12

RESULT 14
US-09-864-761-34868
; Sequence 34868, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomico-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34868
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006977.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.3
; OTHER INFORMATION: SWISSPROT HIT: P00533, EVALUATE 9.00e-10
; OTHER INFORMATION: EST_HUMAN HIT: BE744284.1, EVALUATE 1.00e-08
US-09-864-761-34868

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Best Local Similarity 95.8%; Score 23; DB 10; Length 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
Db 16 LLLVIA 21

RESULT 15
US-10-001-870-116
; Sequence 116, Application US/10001870
; Patent No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Saiceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 116
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-870-116

Query Match
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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2003, 15:21:45 : Search time 26.5909 Seconds
(without alignments)
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Title: US-09-543-188a-13
Perfect score: 24
Sequence: 1 LLVIA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	100.0	6	23	AAU11836
2	24	100.0	42	21	AAB34100
3	24	100.0	67	21	AAG61661
4	24	100.0	93	23	ABP05389
5	24	100.0	140	23	ABB90320
6	24	100.0	173	23	ABP39430
7	24	100.0	179	22	ABBI0539
8	24	100.0	179	22	AAU18139
9	24	100.0	179	22	AAU18690
10	24	100.0	179	22	AAU17055

11	24	100.0	182	21	AAG10813	Arabidopsis thalia
12	24	100.0	182	21	AAG42630	Arabidopsis thalia
13	24	100.0	183	21	AAG10812	Arabidopsis thalia
14	24	100.0	183	21	AAG42629	Arabidopsis thalia
15	24	100.0	271	22	AAU45545	Proionibacterium
16	24	100.0	283	22	ABG06298	Novel human diago
17	24	100.0	296	21	AAB42264	Human ORFX ORF2010
18	24	100.0	327	22	ABG82005	S. epidermidis ope
19	24	100.0	329	23	ABB91800	Herbivore-derived activ
20	24	100.0	346	22	ABB52990	Escherichia coli p
21	24	100.0	447	23	ABP28635	Streptococcus poly
22	24	100.0	478	22	AAU16984	Human novel secret
23	24	100.0	485	21	AAB59032	Breast and ovarian
24	24	100.0	487	22	ABB10372	Human CDNA SEQ ID
25	24	100.0	491	23	ABB81636	Human zcytor19 pro
26	24	100.0	504	22	AAG90281	C glutamicum prote
27	24	100.0	520	23	ABB81643	Human zcytor19 pro
28	24	100.0	575	21	AAV71080	Murine TANGO 136 p
29	24	100.0	591	20	AAV15228	Human receptor pro
30	24	100.0	630	23	ABP39770	Staphylococcus epi
31	24	100.0	688	22	AAU93311	Human polypeptide,
32	24	100.0	713	20	AAV41712	Human PRO724 prote
33	24	100.0	713	21	AAB44268	Human PRO724 (UNQ3
34	24	100.0	713	21	AAV71081	Human TANGO 136 pr
35	24	100.0	713	22	AAU29231	Human PRO polypept
36	24	100.0	713	23	ABB95462	Human angiogenesis
37	24	100.0	713	23	ABB90346	Human polypeptide
38	24	100.0	713	23	ABB84856	Human PRO724 prote
39	24	100.0	713	23	ABB05751	Human G protein-co
40	24	100.0	814	22	ABG04441	Novel human diago
41	24	100.0	840	22	AAB70544	Human PRO14 protei
42	24	100.0	859	20	AAV02381	Polypeptide identi
43	24	100.0	859	21	AAB42317	Human ORFX ORF2081
44	24	100.0	859	22	AAU24052	Human EST encoded
45	24	100.0	859	22	AAU14316	Human novel protei

ALIGNMENTS

RESULT 1
ID AAU11836 standard; peptide: 6 AA.
AC AAU11836;
XX 26-MAR-2002 (first entry)
XX
DE Peptide ligand for Prion protein, PrP. #11.
XX
KW Prion protein; PrP; ligand: octapeptide motif; scrapie;
KW prion-associated disease; Creutzfeldt-Jakob disease;
KW Gerstmann-Strausler-Scheinker disease; fatal familial
KW transmissible spongiform encephalopathy; bovine spongiform encephalopathy;
KW chronic wasting disease.
XX
OS Synthetic.
XX
PN WO200177687-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-0511150.
XX
PR 05-APR-2000; 2000US-0543188.
XX
PA (VITE-) VI TECHNOLOGIES INC.
XX
PI Hammond DJ, Wiltshire VR, Carbonell R, Shen H;
XX WPI, 2002-061944/08.
XX

PT New ligands for prion proteins, useful for detection or removal or
PT prions and for treating prion-associated diseases, recognize a specific
PT octapeptide motif -

XX Claim 16: Page 34; 47pp; English.

CC The invention relates to a ligand of less than 6 kD that binds to a
CC polypeptide containing the sequence GLYTYRGLYGLNProHISGLYGLY (A) or an
CC analogue that is the retro-inverse isomer of (A). The sequence A is
CC an octapeptide motif from the prion protein (PrP). The ligands are
CC identified by binding assays with the peptide (A) or peptides containing
CC (A). The ligands are used for detecting prion proteins (or prions) in
CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jakob diseases (in
CC iatrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strausner-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is a ligand of the invention.

Sequence 6 AA:

Query Match 100.0%; Score 24; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
1 LLLVIA 6
DB 1 LLLVIA 6

RESULT 2
AAB34100

ID AAB34100 standard; Protein: 42 AA.

AC AAB34100;

DT 26-JAN-2001 (first entry)

DE Human secreted protein sequence encoded by gene 9 SEQ ID NO:68.

XX Human; secreted protein; diagnosis; antiarthritic; immunosuppressive;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotrophic;
KW cerebroprotective; neotrophic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; vulnery; gene therapy; autoimmune disease;
KW hyperproliferative disorder; neoplasm; cancer; cardiovascular disorder;
KW cerebrovascular disorder; angiogenesis; nervous system disorder;
KW infection; ocular disorder; wound healing; skin aging; food additive;
XX preservative.

OS Homo sapiens.

PN WO200056755-A1.

PD 28-SEP-2000.

PF 16-MAR-2000; 2000KO-US06830.

PR 19-MAR-1999; 99US-0125361.

PR 10-DEC-1999; 99US-0169910.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsoulis G;

DR WPI: 2000-587661/55.

DR N-PSDB: AAC59457.

XX New isolated nucleic acid molecules encoding 49 human secreted proteins
PT used for preventing, treating or ameliorating medical conditions, for
PT diagnosing pathological conditions or as food additives or
PT preservatives

XX Claim 11: Page 366; 419pp; English.

CC The polynucleotide sequences given in AAC59449 to AAC59497 encode the
CC human secreted proteins given in AAB34092 to AAB34140. AAB34141 to
CC AAB34216 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissue
CC and cells the genes are expressed in. Examples of activities include:
CC antirheumatic; immunosuppressive; antirheumatic; antiproliferative;
CC cytostatic; cardiant; vasotropic; cerebroprotective; neotrophic;
CC neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
CC and vulnery. The polynucleotides and polypeptides can be used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms or
CC cancer of the breast or liver, cardiovascular disorders, cerebrovascular
CC disorders, angiogenesis, nervous system disorders, infections caused by
CC bacteria, viruses and fungi and ocular disorders. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities. AAC59440 to AAC59448 and AAB34091 represent sequences used
CC in the exemplification of the present invention.

Sequence 42 AA:

Query Match 100.0%; Score 24; DB 21; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
1 LLLVIA 6
DB 3 LLLVIA 8

RESULT 3
AAG61661

ID AAG61661 standard; Protein: 67 AA.

AC AAG61661;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 80003.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157733.
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PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
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PR 14-OCT-1999; 99US-0159638.
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PR 21-OCT-1999; 99US-0160768.
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PR 21-OCT-1999; 99US-0160815.
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PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 24; DB 21; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 12 LLLVIA 17

RESULT 4
ABP05389

ID ABP05389 standard; Protein; 93 AA.

AC ABP05389;

DT 25-JUN-2002 (first entry)

DE Human ORFX protein sequence SEQ ID NO:10760.

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
hyperproliferative disorder; psoriasis; benign tumour; hemorrhage;
degenerative disorder; osteoarthritis; neurodegenerative disorder;
cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
hypertension; hypothyroidism; cholesterol ester storage disease;
immune deficiency; immune disorder; infectious disease;
autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
myasthenia gravis.

KM Homo sapiens.

WO200192523-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US10836.

30-MAY-2000; 2000US-206132P.

29-AUG-2000; 2000US-228716P.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach MD;

WPI; 2002-106308/14.

N-PSDB; ABN21141.

Novel human polypeptides and polynucleotides useful for diagnosing,
preventing and treating cardiovascular disease, neurodegenerative,
hyperproliferative disorders and autoimmune disorders

XX
PS Disclosure: SEQ ID 10760; 1037pp; English.

CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 93 AA:

Query Match 100.0%; Score 24; DB 23; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 19 LLLVIA 24

RESULT 5
ABB90320

ID ABB90320 standard; Protein; 140 AA.

AC ABB90320;

DT 24-MAY-2002 (first entry)

DE Human polypeptide SEQ ID NO 2696.

Cytostatic; immunosuppressive; nontropic; neuroprotective; antiviral;
antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
neurological disease; infection; human; secreted protein.

KM Homo sapiens.

WO200190304-A2.

29-NOV-2001.

18-MAY-2001; 2001WO-US16450.

19-MAY-2000; 2000US-205515P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-122018/16.

N-PSDB; ABL90729.

PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX Claim 11; SEQ ID NO 2696; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AB189449-AB190853) and proteins
CC (AB889040-AB890444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast; gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial infarction;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 140 AA:
Query Match 100.0%; Score 24; DB 23; Length 140;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLLVIA 6
Db 95 LLLVIA 100
RESULT 6
ABP39430
ID ABP39430 standard; Protein: 173 AA.
XX
AC ABP39430;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4275.
XX
XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
XX US6380370-B1.
XX
PN 30-APR-2002.
XX
PD 13-AUG-1998; 98US-0134001.
XX
PE 14-AUG-1997; 97US-055779P.
XX
PR 08-NOV-1997; 97US-064964P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
PA Doucette-Stamm LA, Bush D;
XX
PI WPI; 2002-381255/41.
XX
DR N-PSDB; ABN91975.
XX
XX Novel isolated nucleic acid encoding a Staphylococcus epidermidis
PT polypeptide, useful for diagnosing and treating bacterial infections -
XX
PS Disclosure; SEQ ID 4275; 267pp; English.
XX

CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences
CC can also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life
CC cycle or inhibit S. epidermidis infection.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.
XX
SQ Sequence 173 AA:
Query Match 100.0%; Score 24; DB 23; Length 173;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLLVIA 6
Db 28 LLLVIA 33
RESULT 7
ABBI0539
ID ABBI0539 standard; Protein: 179 AA.
XX
AC ABBI0539;
XX
DT 10-JAN-2002 (first entry)
XX
XX Human cDNA SEQ ID NO: 847.
DE
XX
XX Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
XX proliferative disorder; inflammation.
XX
OS Homo sapiens.
XX
XX WO200154474-A2.
XX
PN 02-AUG-2001.
XX
PD 17-JAN-2001; 2001MO-US01349.
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PE 31-JAN-2000; 2000US-179065P.
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PR 04-FEB-2000; 2000US-180628P.
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PR 26-JUL-2000; 2000US-220964P.
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PR	08-NOV-2000	2000US-2465583

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XX 08-NOV-2000; 2000US-246609P.
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PR 17-NOV-2000; 2000US-249210P.
PR 17-NOV-2000; 2000US-249211P.
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PR 17-NOV-2000; 2000US-249218P.
PR 17-NOV-2000; 2000US-249244P.
PR 17-NOV-2000; 2000US-249245P.
PR 17-NOV-2000; 2000US-249264P.
PR 17-NOV-2000; 2000US-249265P.
PR 17-NOV-2000; 2000US-249297P.
PR 17-NOV-2000; 2000US-249299P.
PR 17-NOV-2000; 2000US-249300P.
PR 01-DEC-2000; 2000US-250160P.
PR 01-DEC-2000; 2000US-250391P.
PR 05-DEC-2000; 2000US-251030P.
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PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
PR 08-DEC-2000; 2000US-251989P.
PR 08-DEC-2000; 2000US-251990P.
PR 11-DEC-2000; 2000US-254097P.
PR 05-JAN-2001; 2001US-259678P.

(PHMA-) HUMAN GENOME SCT INC.
XX
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX DR WPI: 2001-476161/51.
XX DR N-PSDB: ABA06761.
XX
XX PT Isolated nucleic acid molecule encoding an inflammation-associated
XX PT polypeptide is used in preventing, treating or ameliorating a medical
XX PT condition _
XX
XX CS Claim 11; SEQ ID NO: 847; 859pp + Sequence Listing: English.
XX
XX CC The present invention provides human cDNAs, proteins and related genomic
XX CC DNAs. These can be used in the treatment of neural, immune system,
XX CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX CC renal and proliferative disorders and inflammation. The present sequence
XX CC is a protein of the invention.
XX
XX SQ Sequence 179 AA;
XX
XX Query Match 100.0%; Score 24; DB 22; Length 179;
XX Best Local Similarity 100.0%; Pred. NO. 6.6e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 LLLVIA 6
XX |||||
XX Db 134 LLLVIA 139
XX
XX RESULT 8
XX ID AAU18139 standard; Protein: 179 AA.
XX
XX AC AAU18139;
XX

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DT 21-NOV-2001 (first entry)
XX Novel human uterine motility-association polypeptide #46.
DE
XX Human; uterine motility-association disorder; uterus; pregnancy;
KW labour; menstrual cycle; gene therapy.
XX Homo sapiens.
OS
XX WO200155201-A1.
PN
XX 02-AUG-2001.
PD
XX 17-JAN-2001; 2001WO-US01317.
PF
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205315.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX
DR WPI: 2001-488787/53.
DR N-PSDB: AAS30211.
XX
XX
PT New polynucleotides and polypeptides, useful for diagnosing, treating,
PT preventing or prognosing e.g. kidney, cardiovascular, blood,
PT electrolyte imbalance or neoplastic disorders, autoimmune diseases,
PT cancers

XX
PS Claim 1; SEQ ID NO 129; 506bp; English.
XX
CC The invention relates to novel nucleic acids and polypeptides useful for
CC diagnosing, treating, preventing and/or prognosing disorders related to
CC these polypeptides. The polynucleotides are especially useful in the
CC diagnosis, prognosis, prevention and/or treatment of diseases which
CC include kidney disorders (e.g. renal failure or nephritis),
CC cardiovascular disorders (e.g. hypertension or myocardial infarction),
CC blood disorders (e.g. anaemia or blood coagulation disorders),
CC electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia),
CC neoplastic disorders (e.g. nephroma or renal cell cancer), autoimmune
CC diseases, cancers, inflammatory diseases, reproductive system
CC disorders, endocrine disorders, neural activity and neurological
CC disorders, wound healing and respiratory disorders. AAU1664-AAU18715
CC represent the novel human renal and cardiovascular-associated amino
CC acid sequences of the invention. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at:
CC ftp.wipo.int/pub/published_pcl_sequences.
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SQ Sequence 179 AA;
Query Match 100.0%; Score 24; DB 22; Length 179;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 134 LLLVIA 139
RESULT 10
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ID AAU17055 standard; Protein: 179 AA.
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AC AAU17055;
XX
DT 07-NOV-2001 (first entry)
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XX
DE Human novel secreted protein, SEQ ID 296.
XX
XX
KW Human: immunosuppressive; antiarthritic; antirheumatic;
KW cytosstatic; cardiast; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW vulnerrary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
XX
OS Homo sapiens.
XX
XX
PN MO200155441-A2.
XX
PD 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01320.
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PR	17-NOV-2000	2000US-0249214.</

CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. rheinoids of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 100.0%; Score 24; DB 22; Length 179;
Best Local Similarity 100.0%; Pred. No. 6,6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11

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XX AAG10813;

DF 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 9285.

KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

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KW termination sequence.
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XX Arabidopsis thaliana.
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DT 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.

XX AAU45545;

27-FEB-2002 (first entry)

Propionibacterium acnes immunogenic protein #6441.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2.

01-NOV-2001.

20-APR-2001; 2001WO-US12865.

21-APR-2000; 2000US-199047P.

02-JUN-2000; 2000US-208841P.

07-JUL-2000; 2000US-216747P.

(CORI-) CORIXA CORP.

Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

L'maisonneuve J, Zhang Y, Jen S, Carter D;

WPI; 2001-616774/71.

N-PSDB; AAS59526.

Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Claim 3; SEQ ID NO 6740; 1069pp; English.

Sequences AAU939105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 271 AA;

Query Match 100.0%; Score 24; DB 22; Length 271;

Best Local Similarity. 100.0%; Pred. No. 1e+03; 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 1 LLLVIA 6

Db 47 LLLVIA 52

Search completed: January 3, 2003, 15:28:38
Job time : 27.5909 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:00 ; Search time 9.95455 Seconds
(without alignments)
57.944 Million cell updates/sec

Title: US-09-543-188a-13

Perfect score: 24

Sequence: 1 LLLVIA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	150	2 C71515	probable 15kda cys
2	24	100.0	152	2 F43584	15k cysteine-rich
3	24	100.0	159	2 D82812	hypothetical prote
4	24	100.0	183	2 G84609	hypothetical prote
5	24	100.0	224	2 T32185	hypothetical prote
6	24	100.0	232	2 C72609	hypothetical prote
7	24	100.0	239	2 T36065	probable integral
8	24	100.0	276	1 PWYBAA	H+-transporting tw
9	24	100.0	277	2 T29611	hypothetical prote
10	24	100.0	281	2 S74551	hypothetical prote
11	24	100.0	284	2 S22414	signal peptidase I
12	24	100.0	284	2 H83550	probable signal pe
13	24	100.0	295	2 G98301	hypothetical ABC t
14	24	100.0	295	2 A12981	ABC transporter, m
15	24	100.0	295	2 AD0306	probable membrane
16	24	100.0	296	2 T12469	hypothetical prote
17	24	100.0	297	2 S75656	hypothetical prote
18	24	100.0	301	2 H97505	probable nKc prot
19	24	100.0	301	2 AD2724	ABC transporter, m
20	24	100.0	316	2 T31880	hypothetical prote
21	24	100.0	326	2 B71644	undecaprenyl-phosp
22	24	100.0	349	2 T00525	probable GST-moti
23	24	100.0	361	2 G72636	hypothetical prote
24	24	100.0	375	2 H86938	conserved hypotet
25	24	100.0	392	2 D70475	conserved hypotet
26	24	100.0	428	2 D70583	probable transmemb
27	24	100.0	437	2 S73284	probable transmemb
28	24	100.0	464	2 E64060	p1b protein homol
29	24	100.0	487	2 E70480	probable sodium/pr

30	24	100.0	509	2 A57512	beta-glucosidase B
31	24	100.0	601	2 E95296	probable ABC-type
32	24	100.0	654	2 G84153	hypothetical prote
33	24	100.0	726	2 S50833	holocarboxylase sy
34	24	100.0	770	2 T00204	LDL receptor relat
35	24	100.0	770	2 T00203	LDL receptor relat
36	24	100.0	896	2 AB1156	conserved membrane
37	24	100.0	896	2 AE1514	conserved membrane
38	24	100.0	1011	2 T45718	receptor-kinase 11
39	24	100.0	1239	2 T42020	class IV chitin sy
40	24	100.0	1266	2 T22090	hypothetical prote
41	23	95.8	50	2 D72804	gp38 protein - Myc
42	23	95.8	73	2 AB3444	hypothetical prote
43	23	95.8	100	2 T43116	hypothetical prote
44	23	95.8	104	2 AC0162	probable membrane
45	23	95.8	105	2 F70545	hypothetical prote

ALIGNMENTS

RESULT 1
C71515
probable 15kda cysteine-rich protein - Chlamydia trachomatis (serotype D, strain UW3/
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 10-Dec-1999
C:Accession: C71515
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A:Reference number: A71570; WUID:99000809; PMID:9784136
A:Accession: C71515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <ARN>
A:Cross-references: GB:AE001317; GB:AE001273; NID:93328663; PIDN:AA68041.1; PID:9332
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: crpA
C:Superfamily: Chlamydia 15k cysteine-rich outer membrane protein

Query Match 100.0%; Score 24; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
Db 48 LLLVIA 53

RESULT 2
F43584
15k cysteine-rich outer membrane protein - Chlamydia trachomatis (serotype C)
C:Species: Chlamydia trachomatis
C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 10-Dec-1999
C:Accession: F43584; S24274
R:de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Marroff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1196-1201, 1991
A:Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodal
A:Reference number: A43584; WUID:91147205; PMID:19974723
A:Accession: F43584
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152
A:Cross-references: EMBL:X54388; NID:940760; PIDN:CAA38258.1; PID:940762
C:Superfamily: Chlamydia 15k cysteine-rich outer membrane protein
C:Keywords: membrane protein

Query Match 100.0%; Score 24; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6

Db 50 LLLVIA 55
|||||

RESULT 3

D82812

hypothetical protein XF0383 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82812

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; PMID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82812

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-159 <SIM>

A:Cross-references: GB:AE003890; GB:AE003849; NID:g9105215; PIDN:AAF83193.1; GSPDB:GN001

Experimental source: strain 9a5c

Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.; A

Brites, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carter, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kiteajima, J.P.; Klieger, J.E.; Kurame, E.E.; Laist

chdo, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, G.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0383

Query Match 100.0%; Score 24; DB 2; Length 159;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
|||||

Db 53 LLLVIA 58

RESULT 4

609

hypothetical protein AC292170 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: G84609

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shaa, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: G84609

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-183 <STO>

A:Cross-references: GB:AE002093; NID:g4567207; PIDN:AAD23623.1; GSPDB:GN00139

C:Genetics:

A:Gene: AC292170

A:Map position: 2

Query Match 100.0%; Score 24; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6

Db 12 LLLVIA 17
|||||

RESULT 5

T32185

hypothetical protein ZK994.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T32185

R:Davidson, S.; Wohldmann, P.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid ZK994.

A:Reference number: Z21133

A:Accession: T32185

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-224 <DAN>

A:Cross-references: EMBL:AF022977; PIDN:AB88611.1; GSPDB:GN00023; CESP:ZK994.4

A:Experimental source: strain Bristol N2; clone ZK994

C:Genetics:

A:Gene: CESP:ZK994.4

A:Map position: 5

A:introns: 42/1; 93/3; 141/3; 188/2

Query Match 100.0%; Score 24; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
|||||

Db 6 LLLVIA 11

RESULT 6

C72609

hypothetical protein APE1337 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: C72609

R:Kawabadyasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; PMID:99310339; PMID:10382966

A:Accession: C72609

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-232 <RAW>

A:Cross-references: DBJ:AP000061; NID:g5104821; PIDN:BAA80329.1; PID:d1044115; PID:g

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1337

Query Match 100.0%; Score 24; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
|||||

Db 82 LLLVIA 87

RESULT 7

T36065

probable integral membrane protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T36065

R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,

submitted to the EMBL Data Library, November 1998

A:Reference number: Z21595

A:Accession: T36065

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-239 <SAU>
A:Cross-references: EMBL:AL034355; PIDN:CAA22231.1; GSPDB:GN00070; SCOPDB:SCD78.26
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOPDB:SCD78.26

Query Match
Best Local Similarity 100.0%; Score 24; DB 2; Length 239;
Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 29 LLLVIA 34

RESULT 8

PHYBAA
transporting two-sector ATPase (EC 3.6.3.14) chain a - Synechocystis sp. (strain PCC 6803)
Alternate names: ATP synthase chain a
C:Species: Synechocystis sp.

A:Variety: PCC 6803
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 14-Dec-2001
C:Accession: S17746; S74588; S14861
R:Li, H.; Nelson, N.
Plant Mol. Biol. 17, 641-652, 1991
A:Title: The atpI and atp2 operons of the cyanobacterium Synechocystis sp. PCC 6803.
A:Reference number: S17745; MUID:92003679; PMID:1832989
A:Accession: S17746
A:Molecule type: DNA

A:Residues: 1-276
A:Cross-references: EMBL:X58128; NID:g47506; PIDN:CAA1130.1; PID:g47508
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74588
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-276 <KAN>
A:Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BA16740.1; PID:g165181
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:

A:Gene: atpI
C:Superfamily: H⁺-transporting ATP synthase protein 6
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; transmembrane protein
F:63-82/Domain: transmembrane #status predicted <TM1>
F:7-44/Domain: transmembrane #status predicted <TM2>
F:122-140/Domain: transmembrane #status predicted <TM3>
F:160-179/Domain: transmembrane #status predicted <TM4>
F:225-242/Domain: transmembrane #status predicted <TM5>
F:247-265/Domain: transmembrane #status predicted <TM6>

Query Match
Best Local Similarity 100.0%; Score 24; DB 1; Length 276;
Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 72 LLLVIA 77

RESULT 9

T29611
hypothetical protein C54H2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T29611
R:Fulton, L.; Gattung, S.
submitted to the EMBL Data Library, May 1996

A:Description: The sequence of C. elegans cosmid C54H2.
A:Reference number: 220651
A:Accession: T29611

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-277 <FOL>
A:Cross-references: EMBL:U58728; PIDN:AAB00591.1; GSPDB:GN00028; CESP:C54H2.5
A:Experimental source: strain Bristol N2; clone C54H2
C:Genetics:
A:Gene: CESP:C54H2.5
A:Map position: X
A:Introns: 23/3; 126/2; 230/2
C:Superfamily: Caenorhabditis elegans hypothetical protein C54H2.5

Query Match
Best Local Similarity 100.0%; Score 24; DB 2; Length 277;
Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 257 LLLVIA 262

RESULT 10

S74551
hypothetical protein slr0241 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.

A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S74551
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-281 <KAN>
A:Cross-references: EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BA16703.1; PID:dl01
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match
Best Local Similarity 100.0%; Score 24; DB 2; Length 281;
Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 264 LLLVIA 269

RESULT 11

S22414
signal peptidase I (EC 3.4.21.89) - Pseudomonas fluorescens
N:Alternate names: leader peptidase 1
C:Species: Pseudomonas fluorescens
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 19-May-2000
C:Accession: S22414
R:Black, M.T.; Munn, J.G.R.; Allsop, A.E.
Biochem. J. 282, 539-543, 1992
A:Title: On the catalytic mechanism of prokaryotic leader peptidase 1.
A:Reference number: S22413; MUID:92189595; PMID:1546569
A:Accession: S22414

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-284 <BLA>

A:Cross-references: EMBL:X56466; NID:g45509; PIDN:CAA39839.1; PID:g45511
C:Superfamily: signal peptidase I
C:Keywords: hydrolase; serine proteinase; transmembrane protein

Query Match
Best Local Similarity 100.0%; Score 24; DB 2; Length 284;
Pred. No. 3.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||

DB 7 LLLVIA 12

RESULT 12

H83550

probable signal peptidase I (EC 3.4.21.89) PA0768 [similarity] - *Pseudomonas aeruginosa*
C:Species: *Pseudomonas aeruginosa*

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 24-May-2001

C:Accession: H83550

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: AB2950; MUID:20437337; PMID:10984043

C:Accession: H83550

C:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-284 <STO>

A:Cross-references: GB:AE004511; GB:AE004091; NID:g9946646; PIDN:AAG04157.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: lepb; PA0768

C:Superfamily: signal peptidase I

C:Keywords: hydrolase; serine proteinase

Query Match 100.0%; Score 24; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||

DB 7 LLLVIA 12

RESULT 13

G98301

hypothetical ABC transporter permease protein yddQ AGR_L_2741 [imported] - *Agrobacterium*
C:Species: *Agrobacterium tumefaciens*

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002

C:Accession: G98301

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*

A:Reference number: A97359; PMID:11743194

A:Accession: G98301

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-295 <KUR>

A:Cross-references: GB:AE007870; PIDN:AAK89937.1; PID:g15159892; GSPDB:GN00170

C:Genetics:

A:Gene: AGR_L_2741

A:Map position: linear chromosome

C:Superfamily: oligopeptide permease protein oppb

Query Match 100.0%; Score 24; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||

DB 39 LLLVIA 44

RESULT 14

A12981

ABC transporter, membrane spanning protein Atu3458 [imported] - *Agrobacterium tumefaciens*
C:Species: *Agrobacterium tumefaciens*

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C:Accession: A12981

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyayin, T.; Levy, R.; Li, M.; McCl

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: A12981

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-295 <KUR>

A:Cross-references: GB:AE008689; PIDN:AA144271.1; PID:g17741857; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu3458

A:Map position: linear chromosome

C:Superfamily: oligopeptide permease protein oppb

Query Match 100.0%; Score 24; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||

DB 39 LLLVIA 44

RESULT 15

AD0306

probable membrane protein YPO2507 [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AD0306

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M

deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G

ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AD0306

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-295 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC91312.1; PID:g15980501; GSPDB:GN00175

A:Gene: YPO2507

Query Match 100.0%; Score 24; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||

DB 17 LLLVIA 22

Search completed: January 3, 2003, 15:33:17
Job time: 10.9545 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:22:10 : Search time 5.18182 Seconds
(without alignments)
48.025 Million cell updates/sec

Title: US-09-543-188a-13
Perfect score: 24
Sequence: 1 LLLVIA 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	96	BV8_BOMVA	Q9PW66 bombina var
2	24	100.0	117	Y13K_BPT4	P39504 bacterioph
3	24	100.0	150	CRPD_CHLTR	O84449 chlamydia t
4	24	100.0	152	CRPC_CHLTR	P26756 chlamydia t
5	24	100.0	162	Y066_GVCL	P41728 cryptophleb
6	24	100.0	276	ATP6_STNY3	P27178 synochocyst
7	24	100.0	277	SUR4_CAEL	Q18864 caenorhabdi
8	24	100.0	284	LEP_PSEAE	Q91597 pseudomonas
9	24	100.0	284	LEP_PSEAE	P26844 pseudomonas
10	24	100.0	415	MNTH_MYCBO	O69443 mycobacteri
11	24	100.0	428	MNTH_MYCBO	O05916 mycobacteri
12	24	100.0	437	YC44_PORPU	P51363 porphyra pu
13	24	100.0	464	HOPE_HAEIN	P44622 haemophilus
14	24	100.0	726	BPL1_HUMAN	P50747 h biotin--P
15	24	100.0	1239	CHS5_USTMA	O13394 ustilago ma
16	24	95.8	50	VG38_BRMD2	O64229 mycobacteri
17	23	95.8	145	Y657_ARCFU	O29600 archaeoglob
18	23	95.8	188	DSBE_YERPE	O82d52 yersinia pe
19	23	95.8	205	Y115_NPVOP	O10354 oryza pseu
20	23	95.8	207	IL6_MARMO	O35736 marmota mon
21	23	95.8	208	IL6_FELCA	P41683 felis silve
22	23	95.8	246	VS09_ROTGI	P30889 rotavirus (
23	23	95.8	269	PTFC_BACST	P26381 bacillus su
24	23	95.8	269	SUR4_FUGRU	O57580 fugu rubrip
25	23	95.8	269	SUR4_HUMAN	O15260 homo sapien
26	23	95.8	269	SUR4_HUMAN	O64310 mus musculi
27	23	95.8	318	FECD_ECOLI	P15029 escherichia
28	23	95.8	334	FECD_ECOLI	P23876 escherichia
29	23	95.8	363	CYA2_RHIME	O52915 rhizobium m
30	23	95.8	425	GSPU_ERMCA	P31708 erwinia car
31	23	95.8	429	SECY_AQUAE	O66491 aquifex aeo
32	23	95.8	430	YBAT_ECOLI	P77400 escherichia
33	23	95.8	499	C831_ARATH	O65782 arabidopsis

34	23	95.8	503	1	AGP4_HUMAN	O9Y264 homo sapien
35	23	95.8	531	1	PTM1_YEAST	P32857 saccharomyc
36	23	95.8	628	1	LU_HUMAN	P50895 homo sapien
37	23	95.8	633	1	NUOL_MYCTU	O86350 mycobacteri
38	23	95.8	704	1	PMA2_LYCES	P23960 lycopersico
39	23	95.8	910	1	DDRI_RAT	O63474 rattus norv
40	23	95.8	911	1	DDRI_MOUSE	O03146 mus musculu
41	23	95.8	913	1	DDRI_HUMAN	O08345 h epithelia
42	23	95.8	956	1	PMA3_NICPL	O08436 nicotiana p
43	23	95.8	962	1	YS96_CAEL	O09965 caenorhabdi
44	23	95.8	1047	1	ANPB_BOVIN	P46197 bos taurus
45	23	95.8	1047	1	ANPB_RAT	P16067 rattus norv

ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	96 AA
BV8_BOMVA				
AC	Q9PW66			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Protein BV8 precursor.			
OS	Bombina variegata (Yellow-bellied toad).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.			
OX	NCBI_TaxID=8348;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=SKIN.			
RX	MEDLINE=9349621; PubMed=10422759;			
RA	Mollay C., Wechseltberger C., Mignogna G., Negri L., Melchiorri P.,			
RA	Barra D., Kreil G.;			
RT	Bv8, a small protein from frog skin and its homologue from snake			
RT	venom induce hyperalgesia in rats.;			
RL	Eur. J. Pharmacol. 374:189-196(1999).			
CC	- FUNCTION: Potentially contract gastrointestinal (GI) smooth muscle.			
CC	- INDUCES hyperalgesia.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- SIMILARITY: BELONGS TO THE PROKINECTIN FAMILY.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
DR	EMBL: AF168790; AAD45816.1; -			
DR	HSSP: P25687; 1IMT.			
KW	Signal.			
FT	CHAIN 1 19			
FT	DISULFID 26 38			
FT	DISULFID 32 50			
FT	DISULFID 37 78			
FT	DISULFID 60 86			
FT	DISULFID 80 95			
FT	SEQUENCE 96 AA; 10102 MW; A12490A7437609B4 CRC64;			
QY	1 LLLVIA 6			
QY				
Db	10 LLLVIA 15			
RESULT 2				

Y13K_BP74
ID Y13K_BP74 STANDARD; PRT; 117 AA.
AC P39504;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical 13.1 kDa protein in pser-alc intergenic region.
GN Y13K OR PSET.3.
OS Bacteriophage T4.
OC Viruses: dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OC NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RA Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RA Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
RT "Bacteriophage T4 genome analysis.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

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CC EMBL: AF158101; AAD42645.1; -
CC DR Hypothetical protein.
CC KW
SQ SEQUENCE 117 AA; 13135 MW; D8B52577D7DA979B CRC64;

Query Match 100.0%; Score 24; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVIA 6
| | | | |
Db 11 LLVIA 16

RESULT 3
CRPD_CHLTR STANDARD; PRT; 150 AA.
AC 084449;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 15 kDa cysteine-rich outer membrane protein, serovar D.
GN CRPA OR CT442.
OS Chlamydia trachomatis.
OC Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
OC NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=D/UN-3/CX;
RA MEDLINE=9000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
-i- FUNCTION: ASSOCIATED WITH DIFFERENTIATION OF RETICULATE BODIES
(RBS) INTO ELEMENTARY BODIES (EBs). IT IS NECESSARY FOR STRUCTURAL
INTEGRITY OF THE EBS OUTER ENVELOPE.
-i- SUBCELLULAR LOCATION: Outer membrane.

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CC or send an email to license@isb-sib.ch.
CC EMBL: AE001317; AAC68041.1; -
DR Outer membrane: Complete proteome.
SQ SEQUENCE 150 AA; 15985 MW; 77A6FB7CC8FAD34 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVIA 6
| | | | |
Db 48 LLVIA 53

RESULT 4
CRPD_CHLTR STANDARD; PRT; 152 AA.
ID Y096_GVCL
AC P26756;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 15 kDa cysteine-rich outer membrane protein, serovar C.
GN CRPA.
OS Chlamydia trachomatis.
OC Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
OC NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C/TW-3;
RA MEDLINE=91147205; PubMed=1997423;
RA de la Maza L.M., Fiedler T.J., Carlson E.J., Markoff B.A.,
RA Peterson E.M.;
RT "Sequence diversity of the 60-kilodalton protein and of a putative
RT 15-kilodalton protein between the trachoma and lymphogranuloma
RT venereum biovars of Chlamydia trachomatis.";
RL Infect. Immun. 59:1196-1201(1991).
-i- FUNCTION: ASSOCIATED WITH DIFFERENTIATION OF RETICULATE BODIES
(RBS) INTO ELEMENTARY BODIES (EBs). IT IS NECESSARY FOR STRUCTURAL
INTEGRITY OF THE EBS OUTER ENVELOPE.
-i- SUBCELLULAR LOCATION: Outer membrane.

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CC EMBL: X54388; CAA38258.1; -
CC DR PIR: F43584; F43584.
CC KW Outer membrane.
SQ SEQUENCE 152 AA; 16133 MW; 31D325CC0619A2F1 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVIA 6
| | | | |
Db 50 LLVIA 55

RESULT 5
Y096_GVCL
ID Y096_GVCL STANDARD; PRT; 162 AA.
AC P41728;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 18.6 kDa protein in P143-LF5 intergenic region.
OS Cryptophlebia leucotreta granulosis virus (ClGV) (Cryptophlebia

OS leucotreta granulovirus).
CC VIRUSES: dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=35254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292936; PubMed=8021613;
RA Jehle J.A., Backhaus H.;
RT "Genome organization of the DNA-binding protein gene region of
RT Cryptophlebia leucotreta granulosis virus is closely related to that
RT of nuclear polyhedrosis viruses";
RL J. Gen. Virol. 75:1815-1820(1994).
CC -1- SIMILARITY: TO CORRESPONDING ORF IN ACMPV AND OPMNV.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
CC -----
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CC -----
CC EMBL: X77048; CAA54340.1; -
CC KW Hypothetical protein.
SQ SEQUENCE 162 AA; 18556 MW; 97C75FD0DE9FP88 CRC64;
Query Match 100.0%; Score 24; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLVIA 6
Db 9 LLLVIA 14

RESULT 6
ATP6, SYN3
ID ATP6, SYN3 STANDARD; PRT; 276 AA.
AC P27178;
DT 01-ANG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase A chain (EC 3.6.3.14) (Protein 6).
GN ATPB OR ATP1 OR SLI1322.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
[1]
SEQUENCE FROM N.A.
RA Lill H., Nelson N.; PubMed=1832989;
RT "The atp1 and atp2 operons of the cyanobacterium Synechocystis sp.
RT PCC 6803.";
RL Plant Mol. Biol. 17:641-652(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
CC H(+) (out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 8
CC POTENTIAL TRANSMEMBRANE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
CC -----
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CC -----
CC EMBL: X58128; CAA41130.1; -
CC DR EMBL: D90900; BAA16740.1; -
CC DR PIR: S17746; PWTBA.
CC DR InterPro: IPR000568; ATPsyn_Asub.
CC DR Pfam: PF00119; ATP-synt_A; 1.
CC DR PRINTS: PR00123; ATPASEA.
CC DR TIGRFS: TIGR01131; ATP-synt_6_of_A; 1.
CC DR PROSITE: PS00449; ATPASE_A; 1.
CC KW Hydrogen ion transport; CF(0); Transmembrane; Complete proteome.
FT TRANSMEM 27 44 POTENTIAL.
FT TRANSMEM 63 82 POTENTIAL.
FT TRANSMEM 122 140 POTENTIAL.
FT TRANSMEM 160 179 POTENTIAL.
FT TRANSMEM 225 242 POTENTIAL.
FT TRANSMEM 247 265 POTENTIAL.
SQ SEQUENCE 276 AA; 30698 MW; E65B9DE31C7621FF CRC64;
Query Match 100.0%; Score 24; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLVIA 6
Db 72 LLLVIA 77

RESULT 7
SUR4, CAEEL
ID SUR4, CAEEL STANDARD; PRT; 277 AA.
AC Q18864; Q18006;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Surfeit locus protein 4 homolog.
GN SURF-4 OR C54H2.5.
OS Caenorhabditis elegans.
OC Caenorhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditioidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=96413309; PubMed=8816471;
RA Ames N., Fried M.;
RT "Surfeit locus gene homologs are widely distributed in invertebrate
RT genomes.";
RL Mol. Cell. Biol. 16:5591-5596(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX SRRAIN-Bristol N2;
RA Fulton L., Gatlung S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (by similarity).
CC -1- SIMILARITY: BELONGS TO THE SURF4 FAMILY.
CC -----
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CC -----
CC DR EMBL; U58728; AAB0591.1; -.
CC DR EMBL; Y14949; CAA75173.1; -.
CC DR WormPeP; C54H2.5; CE06987.
CC DR InterPro; IPR002995; SURF4.
CC DR Pfam; PF02077; SURF4.1.
CC DR PRODOM; PD010195; SURF4.1.
CC DR PROSITE; PS01339; SURF4.1.
CC KW Transmembrane; Endoplasmic reticulum.
CC FT TRANSMEM 71 91 POTENTIAL.
CC FT TRANSMEM 97 117 POTENTIAL.
CC FT TRANSMEM 118 138 POTENTIAL.
CC FT TRANSMEM 163 183 POTENTIAL.
CC FT TRANSMEM 187 207 POTENTIAL.
CC FT TRANSMEM 213 233 POTENTIAL.
CC FT TRANSMEM 250 270 POTENTIAL.
CC FT SITE 274 275 POTENTIAL.
CC FT ENDOPLASTIC RETICULUM RETRIEVAL MOTIF
CC (POTENTIAL).
CC CONFLICT 17 17 A -> R (IN REF. 1).
CC SEQUENCE 277 AA; 31813 MW; 8FF2848676CC0245 CRC64;
CC -----
QY 1 LLVIA 6
QY |||||
DB 257 LLVIA 262
CC -----
RESULT 8
LEP_PSEAE
ID LEP_PSEAE STANDARD; PRT; 284 AA.
AC 0915G7.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Signal peptidase I (EC 3.4.21.89) (Spase I) (Leader peptidase I).
GN LEPA OR PA0768.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_taxid=287;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RC MEDLINE=20437337; Pubmed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Birkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Gader R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1 CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
CC secreted and periplasmic proteins precursor.
CC -1 SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S26; ALSO KNOWN AS TYPE
CC I LEADER PEPTIDASE FAMILY.
CC -----
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CC -----
CC EMBL; AE004511; AAG04157.1; -.

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DR	HSSP: P00803; 1B12.
DR	InterPro: IPR000508; SigPbase.
DR	InterPro: IPR000223; SigPbase_S26A.
DR	Pfam: PF00461; Peptidase_S26; 1.
DR	PRINTS: PR00727; LEADERPTASE.
DR	PROSITE: PS00501; SPASE_I_1; 1.
DR	PROSITE: PS00760; SPASE_I_2; 1.
DR	PROSITE: PS00761; SPASE_I_3; 1.
RW	Inner membrane; Transmembrane; Hydrolase; Protease; Complete proteome.
FT	TRANSMM 4 22 POTENTIAL.
FT	DOMAIN 23 58 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 59 77 POTENTIAL.
FT	DOMAIN 78 284 PERIPLASMIC (POTENTIAL).
FT	ACT_SITE 90 90 BY SIMILARITY.
FT	ACT_SITE 145 145 BY SIMILARITY.
SQ	SEQUENCE 284 AA; 32103 MW; ACA143FA8F90EDZC CRC64;
Query Match	100.0%; Score 24; DB 1; Length 284;
Best Local Similarity	100.0%; Pred. NO. 2.le+02;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 LLVIA 6
Dd	7 LLVIA 12
RESULT 9	
LEP_PSEFL	
ID	LEP_PSEFL. STANDARD; PRI: 284 AA.
AC	P26844.
DT	01-AUG-1992 (Rel. 23, Created)
DT	01-AUG-1992 (Rel. 23, Last sequence update)
DT	01-NOV-1995 (Rel. 32, Last annotation update)
DE	Signal peptidase I (EC 3.4.21.89) (Spase I) (leader peptidase I). LEPB.
GN	Pseudomonas fluorescens.
OS	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC	Pseudomonas.
OX	NCBI_TaxID=294; [1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=NCIMB 10586;
RC	MEDLINE=92189595; PubMed=1546969;
RX	Black M.T., Mann J.G.R., Allsop A.E.; "On the catalytic mechanism of prokaryotic leader peptidase I.";
RT	Biochem. J. 282:539-543(1992).
RL	-1- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from secreted and periplasmic proteins precursor. -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane. -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S26; ALSO KNOWN AS TYPE I LEADER PEPTIDASE FAMILY.
CC	-----
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CC	-----
DR	EMBL: X56466; CAA39839.1; .
DR	PIR: S22414; S22414.
DR	HSSP: P00803; 1B12.
DR	MEROPS: S26.001; .
DR	InterPro: IPR000508; SigPbase.
DR	InterPro: IPR000223; SigPbase_S26A.
DR	Pfam: PF00461; Peptidase_S26; 1.
DR	PRINTS: PR00727; LEADERPTASE.
DR	PROSITE: PS00501; SPASE_I_1; 1.
DR	PROSITE: PS00760; SPASE_I_2; 1.
DR	PROSITE: PS00761; SPASE_I_3; 1.
RW	Inner membrane; Transmembrane; Hydrolase; Protease.

FT TRANSMEM 4 22 POTENTIAL.
 FT DOMAIN 23 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 77 POTENTIAL.
 FT DOMAIN 78 284 PERIPLASMIC (POTENTIAL).
 FT ACT_SITE 90 90 BY SIMILARITY.
 FT ACT_SITE 145 145 BY SIMILARITY.
 SQ SEQUENCE 284 AA; 31903 MW; B1B89D956BDA7891 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 284;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
 111111
 DB 7 LLLVIA 12

RESULT 10
 MNTN_MYCBO STANDARD; PRT; 415 AA.
 069443:
 16-OCT-2001 (rel. 40, Created)
 16-OCT-2001 (rel. 40, Last sequence update)
 15-JUN-2002 (rel. 41, Last annotation update)
 DE Probable manganese transport protein mntH (BRAMP) (Fragment).
 GN MNTN.
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 NCBI_TaxID=1765;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN-BG3:
 MEDLINE=98294035; PubMed=9632246;
 RA Agrinof D.D., Krishna S.;
 RT "Metal ion homeostasis and intracellular parasitism."
 RL Microbiol. 28:403-412(1998).
 CC -1- FUNCTION: H(+)-STIMULATED, HIGHLY SELECTIVE, MANGANESE UPTAKE
 CC -1- SYSTEM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE NRAMP FAMILY.
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 DR EMBL: AJ005699; CA06684.1; -;
 DR InterPro: IPR001046; Nramp.
 DR Pfam: PF01566; Nramp; 1.
 DR PRINTS: PR00447; NATRESASCMP.
 DR ProDom: PD001861; Nramp; 1.
 DR TIGRfams: TIGR01197; nramp; 1.
 KW Transport; Symport; Manganese; Transmembrane.
 FT NON_TER 1 1
 FT TRANSMEM 26 46 POTENTIAL.
 FT TRANSMEM 53 73 POTENTIAL.
 FT TRANSMEM 107 127 POTENTIAL.
 FT TRANSMEM 129 149 POTENTIAL.
 FT TRANSMEM 164 184 POTENTIAL.
 FT TRANSMEM 203 223 POTENTIAL.
 FT TRANSMEM 251 271 POTENTIAL.
 FT TRANSMEM 292 312 POTENTIAL.
 FT TRANSMEM 316 336 POTENTIAL.
 FT TRANSMEM 358 378 POTENTIAL.
 FT TRANSMEM 399 >415 POTENTIAL.
 FT NON_TER 415 415
 SQ SEQUENCE 415 AA; 43564 MW; A006ECPAFB3F0DB0 CRC64;
 Query Match 100.0%; Score 24; DB 1; Length 415;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
 111111
 DB 168 LLLVIA 173

RESULT 11
 MNTN_MYCCTU STANDARD; PRT; 428 AA.
 ID MNTN_MYCCTU
 AC 005916;
 15-JUL-1998 (rel. 36, Created)
 15-JUL-1998 (rel. 36, Last sequence update)
 15-JUN-2002 (rel. 41, Last annotation update)
 DE Probable manganese transport protein mntH (BRAMP).
 GN MNTN OR RV0924C OR MT0951 OR MTCY21C12.18C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: H(+)-STIMULATED, HIGHLY SELECTIVE, MANGANESE UPTAKE
 CC -1- SYSTEM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE NRAMP FAMILY.
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 DR EMBL: Z95210; CAB08494.1; -;
 DR EMBL: AE006981; AKK45198.1; ALT_INIT.
 DR TIGR: MT0951; -;
 DR TubercuList: RV0924c; -;
 DR InterPro: IPR001046; Nramp.
 DR Pfam: PF01566; Nramp; 1.
 DR ProDom: PD001861; Nramp; 1.
 DR TIGRfams: TIGR01197; nramp; 1.
 KW Transport; Symport; Manganese; Transmembrane; Complete proteome.
 FT TRANSMEM 33 53 POTENTIAL.
 FT TRANSMEM 60 80 POTENTIAL.
 FT TRANSMEM 114 134 POTENTIAL.
 FT TRANSMEM 136 156 POTENTIAL.

FT TRANSMEM 171 191 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 258 278 POTENTIAL.
FT TRANSMEM 299 319 POTENTIAL.
FT TRANSMEM 322 343 POTENTIAL.
FT TRANSMEM 365 385 POTENTIAL.
FT TRANSMEM 406 426 POTENTIAL.
SQ SEQUENCE 428 AA; 45004 MW; D90CF98756715CD8 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 175 LLLVIA 180

RESULT 12

YCA4_PORPU STANDARD; PRT; 437 AA.
P51363:
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 50.2 kDa protein ycf44 (ORF437).
GN YCF44.
OS Porphyra purpurea.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxId=2787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Avonport;
RA Reich M.E., Munholland J.;
RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
genome";
RL Plant Mol. Biol. Rep. 13:333-335(1995).
CC -1- SIMILARITY: BELONGS TO THE YCF44 FAMILY.

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EMBL: U38804; AAC08249.1;
Chloroplast; Hypothetical protein.
SQ SEQUENCE 437 AA; 50195 MW; 59F02A977B3A1BD9 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 29 LLLVIA 34

RESULT 13
HOFB_HAEIN STANDARD; PRT; 464 AA.
ID HOFB_HAEIN
AC P44622;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein transport protein hofb homolog.
GN HOFB OR HOFB OR HI0298.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.

OX NCBI_TaxId=727;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7342800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.N., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd";
RL Science 269:496-512(1995).
CC -1- SIMILARITY: BELONGS TO THE PULE/DUTE/EXEE/XPSE/XCPR FAMILY.

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EMBL: U32715; AAC1962.1;
DR TIGR; HI0298;
DR InterPro: IPR001482; GSPIL.E.
DR Pfam: PF00437; GSPIL.E; 1.
DR ProDom: PD000739; GSPIL.E; 1.
DR PROSITE: PS00662; T2SP_E; 1.
KW Transport; ATP-binding; Complete proteome.
FT NP_BIND 264 271 ATP (POTENTIAL).
SQ SEQUENCE 464 AA; 52983 MW; 4923156BE45BD6A2 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 384 LLLVIA 389

RESULT 14

BPL1_HUMAN STANDARD; PRT; 726 AA.
ID BPL1_HUMAN
AC P50747; Q09451;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Biotin-protein ligase (EC 6.3.4.-) (Biotin apo-protein ligase)
DE [Includes: Biotin-[methylmalonyl-CoA-carboxyltransferase] ligase
DE (EC 6.3.4.9); Biotin-[propionyl-CoA-carboxylase (ATP-hydrolyzing)]
DE ligase (EC 6.3.4.10) (Holocarboxylase synthetase) (HCS);
DE Biotin-[methylcrotonoyl-CoA-carboxylase] ligase (EC 6.3.4.11);
DE Biotin-[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15)].
GN HLCS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT HCS PRO-237.
RC TISSUE=Liver;
MEDLINE=95144167; PubMed=7842009;
RA Suzuki Y., Aoki Y., Ishida Y., Chiba Y., Iwamatsu A., Kishino T.,
RA Mikawa N., Matsudaira Y., Marisawa K.;
RT "Isolation and characterization of mutations in the human
holocarboxylase synthetase CDNA";
RL Nat. Genet. 8:122-128(1994).

[2]
 RP SEQUENCE FROM N.A.
 RA Ohira M., Seki N., Nagase T., Suzuki E., Nomura N., Ohara O.,
 RA Hattori M., Sakaki Y., Eki T., Murekami Y., Saito T., Ichikawa H.,
 RA Ohki M.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RA Shitaya K., Kudoh J., Minoshima S., Kawasaki K., Nakatch E.,
 RA Shitani A., Asakawa S., Shimizu N.,
 RT "Genomic sequencing of 1.2-Mb region on human chromosome 21q22.2";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A., AND VARIANTS HCS P-237; W-508; M-550 AND S-581.
 RX PubMed=11735028;
 RA Yang X., Aoki Y., Li X., Sakamoto O., Hiratsuka M., Kure S.,
 RA Taheri S., Christensen E., Inui K., Kubota M., Ohita M., Ohki M.,
 RA Kudoh J., Kawasaki K., Shitaya K., Shitani A., Asakawa S.,
 RA Minoshima S., Shimizu N., Narisawa K., Matsubara Y., Suzuki Y.;
 RA "Structure of human holocarboxylase synthetase gene and mutation
 spectrum of holocarboxylase synthetase deficiency.";
 Hum. Genet. 109:526-534(2001).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Matanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
 RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Folley A.,
 RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shitaya K., Kawasaki K., Asakawa S.,
 RA Shitani A., Sakaki Y., Nagamine K., Mitsuyma S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordiek K., Hornischer K., Brandt P.,
 RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Blecker H.,
 RA Ramer J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E.,
 RA Weinmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehnach H., Reinhardt R., Yaspo M.-L.;
 RA "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319(2000).
 RN [16]
 RP SEQUENCE OF 1-92 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98163741; PubMed=9503011;
 RA Dahmane N., Alt Ghezala G., Gossel P., Chamoun Z.,
 RA Dufresne-Zacharia M.C., Lopes C., Rabatel N., Gassanova-Maugenre S.,
 RA Chetoui Z., Abramowski V., Fayet E., Yaspo M.L., Korn B.,
 RA Blouin J.L., Lehnach H., Poustka A., Antonarakis S.E., Smet P.M.,
 RA Creau N., Delabar J.M.;
 RA "Transcriptional map of the 2.5-Mb CBR-ERG region of chromosome 21
 involved in down syndrome.";
 RL Genomics 48:12-23(1998).
 RN [17]
 RP VARIANT HCS PRO-237.
 RX MEDLINE=96125714; PubMed=8541348;
 RA Aoki Y., Suzuki Y., Sakamoto O., Li X., Takahashi K., Chitake A.,
 RA Sakata R., Ohura T., Miyabayashi S., Narisawa K.;
 RT "Molecular analysis of holocarboxylase synthetase deficiency: a
 missense mutation and a single base deletion are predominant in
 Japanese patients.";
 RL Biochim. Biophys. Acta 1272:168-174(1995).
 RN [18]
 RP VARIANT HCS ASN-571.
 RX MEDLINE=96414311; PubMed=8817339;
 RA Dupuis L., Leon-Del-Rio A., Leclerc D., Campeau E., Szeeman L.,
 RA Saudubray J.M., Herman G., Gibson K.M., Gravel R.A.;
 RT "Clustering of mutations in the biotin-binding region of
 holocarboxylase synthetase in biotin-responsive multiple carboxylase
 deficiency.";
 Hum. Mol. Genet. 5:1011-1016(1996).
 RN [19]
 RP VARIANTS HCS PRO-237 AND MEN-550.
 RX MEDLINE=98057254; PubMed=9396568;
 RA Aoki Y., Suzuki Y., Li X., Sakamoto O., Chikaoaka H., Takita S.,

RA Narisawa K.;
 RT "Characterization of mutant holocarboxylase synthetase (HCS): a Km for
 RT biotin was not elevated in a patient with HCS deficiency.";
 RL Pediatr. Res. 42:849-854(1997).
 RN [10]
 RP VARIANT HCS GLU-333; ILE-462; SER-581 AND THR-610 DEL.
 RX MEDLINE=99204600; PubMed=10190325;
 RA Aoki Y., Li X., Sakamoto O., Hiratsuka M., Akashi H., Xu L.,
 RA Briones P., Suomalainen T., Baumgartner E.R., Suzuki Y., Narisawa K.;
 RT "Identification and characterization of mutations in patients with
 holocarboxylase synthetase deficiency.";
 Hum. Genet. 104:143-148(1999).
 RL FUNCTION: POSTTRANSLATIONAL MODIFICATION OF SPECIFIC PROTEIN BY
 ATTACHMENT OF BIOTIN. ACTS ON VARIOUS CARBOXYLASES SUCH AS ACETYL-
 COA-CARBOXYLASE, PYRUVATE CARBOXYLASE, PROPYLONYL COA CARBOXYLASE,
 AND 3-METHYLCROTONYL COA CARBOXYLASE.
 CC CATALYTIC ACTIVITY: ATP + biotin + apo-[methylmalonyl-CoA:pyruvate
 carboxyltransferase] = AMP + diphosphate + [methylmalonyl-
 CoA:pyruvate carboxyltransferase].
 CC CATALYTIC ACTIVITY: ATP + biotin + apo-[propionyl-CoA:carbon-
 dioxide ligase (ADP-forming)] = AMP + diphosphate + [propionyl-
 CoA:carbon-dioxide ligase (ADP-forming)].
 CC CATALYTIC ACTIVITY: ATP + biotin + apo-[3-methylcrotonyl-
 CoA:carbon-dioxide ligase (ADP-forming)] = AMP + diphosphate + [3-
 methylcrotonyl-CoA:carbon-dioxide ligase (ADP-forming)].
 CC CATALYTIC ACTIVITY: ATP + biotin + apo-[acetyl-CoA:carbon-dioxide
 ligase (ADP-forming)] = AMP + diphosphate + [acetyl-CoA:carbon-
 dioxide ligase (ADP-forming)].
 CC SUBUNIT: MONOMER.
 CC SUBCELLULAR LOCATION: Cytoplasmic and mitochondrial.
 CC TISSUE SPECIFICITY: MOSTLY EXPRESSED IN MUSCLE, PLACENTA, IN
 LESSER EXTENT IN THE BRAIN, KIDNEY, PANCREAS, LIVER AND LUNG.
 CC DISASE: DEFECTS IN HCS ARE THE CAUSE OF HOCARCOXYLASE
 SYNTHETASE DEFICIENCY (HCS) (OR BIOTIN-RESPONSIVE MULTIPLE
 CARBOXYLASE DEFICIENCY), AN AUTOSOMAL RECESSIVE DISORDER
 CHARACTERIZED BY METABOLIC KETOACIDOSIS, HYPERAMMONEMIA, EXCRETION
 OF ABNORMAL ORGANIC ACID METABOLITES, AND DERMATITIS. CLINICAL
 AND BIOCHEMICAL SYMPTOMS IMPROVE DRAMATICALLY WITH ADMINISTRATION OF
 BIOTIN.
 CC SIMILARITY: WITH E.COLI BIRA AND OTHER EUKARYOTIC BIOTIN--PROTEIN
 LIGASES.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL: D23672; BAA04902.1; -
 DR EMBL: D67328; BAA13332.1; -
 DR EMBL: AP000697; BAA89434.1; -
 DR EMBL: AP000703; BAA89434.1; JOINED.
 DR EMBL: AP000701; BAA89434.1; JOINED.
 DR EMBL: AP000698; BAA89434.1; JOINED.
 DR EMBL: AB063285; BAB68550.1; -
 DR EMBL: AP001727; BAA95511.1; -
 DR EMBL: AP001726; BAA95510.1; -
 DR EMBL: AJ001864; CAA05056.1; -
 DR GeneW: HGNC:4976; HLCS.
 DR MIM: 253270; -
 DR InterPro: IPR003142; BPL_C.
 DR InterPro: IPR004143; BPL_LiPA_LiPB.
 DR InterPro: IPR004408; BPL_Liase.
 DR Pfam: PF02237; BPL_C.1.
 DR Pfam: PF03099; BPL_LiPA_LiPB.1.
 DR TIGRFAMs: TIGR00121; bira_Liase.1.
 DR Ligase: Multifunctional enzyme. Disease mutation.
 KM SIMILAR LIGASES: SOME, TO AVIDIN.
 FT SIMILAR 563 609 L -> P (IN HCS).
 FT VARIANT 237 /FTID=VAR_005084.
 FT VARIANT 333 333 V -> E (IN HCS; <10% ACTIVITY).

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:24:35 : Search time 20.3182 seconds
(without alignments)
60.846 Million cell updates/sec

Title: US-09-543-188A-13
Perfect score: 24
Sequence: 1 LLLVIA 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	98	13 Q9DGL8	Q9dgl8 gallus gall
2	24	100.0	107	5 Q9NIO1	Q9n101 trypanosoma
3	24	100.0	110	16 Q8XPO9	Q8xpu9 rai1stonia s
4	24	100.0	128	5 Q9NIO2	Q9n1q2 trypanosoma
5	24	100.0	159	16 Q9PGB9	Q9pgb9 xylella fas
6	24	100.0	173	17 Q8TWT8	Q8twz8 methanopyru
7	24	100.0	183	10 Q9SIE7	Q9sie7 arabidopsis
8	24	100.0	193	8 Q9MIU4	Q9miu4 hyphochytr
9	24	100.0	223	8 Q8WET9	Q8wet9 lyonsia hya
10	24	100.0	232	5 Q44086	Q44086 caenorhabdi
11	24	100.0	234	17 Q9YCB9	Q9ycb9 aeropyrum p
12	24	100.0	239	16 Q9ZBX3	Q9zbx3 streptomyce
13	24	100.0	248	2 Q85820	Q85820 actinobacill
14	24	100.0	281	16 P72696	P72696 synechocyst
15	24	100.0	295	16 Q8ZDP9	Q8zdp9 yersinia pe
16	24	100.0	295	16 Q8UAB6	Q8uab6 agrobacteri

17	24	100.0	296	4 Q9UG33	Q9ug33 homo sapien
18	24	100.0	297	16 P74131	P74131 synechocyst
19	24	100.0	301	16 Q8UG43	Q8ug43 agrobacteri
20	24	100.0	306	2 Q93SG5	Q93sg5 corynebacte
21	24	100.0	311	2 Q9F0G9	Q9f0g9 pseudomonas
22	24	100.0	315	11 Q8VG59	Q8vg59 mus musculu
23	24	100.0	316	5 Q16463	Q16463 caenorhabdi
24	24	100.0	317	11 Q8VFP6	Q8vfp6 mus musculu
25	24	100.0	326	16 Q9ZCD2	Q9zcd2 rickettsia
26	24	100.0	329	10 Q64468	Q64468 arabidopsis
27	24	100.0	361	17 Q9YBP9	Q9ybp9 aeropyrum p
28	24	100.0	368	10 Q9SXN7	Q9sxn7 nicotiana t
29	24	100.0	375	16 Q9CD53	Q9cd53 mycobacteri
30	24	100.0	392	16 Q67832	Q67832 aquifex aeo
31	24	100.0	410	11 Q923Z0	Q923z0 mus musculu
32	24	100.0	424	16 Q9AK38	Q9ak38 streptomyce
33	24	100.0	427	2 Q9EUD4	Q9eud4 pseudomonas
34	24	100.0	442	16 Q8RGE7	Q8rgf7 fusobacteri
35	24	100.0	445	16 Q9A164	Q9a164 streptococc
36	24	100.0	469	2 Q9JRM9	Q9jrm9 actinobacil
37	24	100.0	487	16 Q67873	Q67873 aquifex aeo
38	24	100.0	497	16 Q98M07	Q98m07 rhizobium l
39	24	100.0	509	10 Q40025	Q40025 hordeum vul
40	24	100.0	601	16 Q930C1	Q930c1 rhizobium m
41	24	100.0	654	16 Q9K5Q7	Q9k5q7 bacillus ha
42	24	100.0	672	6 Q9BE74	Q9be74 macaca fasc
43	24	100.0	689	10 Q8S0A9	Q8s0a9 oryza sativ
44	24	100.0	696	2 Q54201	Q54201 streptomyce
45	24	100.0	713	11 Q9EP88	Q9ep88 mus musculu

ALIGNMENTS

RESULT 1
ID Q9DGL8 PRELIMINARY: PRT: 98 AA.
AC Q9DGL8:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Jun-suppressed chemokine.
JSC.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FIBROBLAST;
RA Harli M., Bister K.;
RT "Suppression of genes in jun-transformed avian fibroblasts."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF285876; AAC00529.1; -
SQ SEQUENCE 98 AA; 11564 MW; 30D88E540ADD55B CRC64;
Query Match 100.0%; Score 24; DB 13; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLVIA 6
DB 9 LLLVIA 14
RESULT 2
ID Q9NIO1 PRELIMINARY: PRT: 107 AA.
AC Q9NIO1:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE Mucin-like protein.
GN SMUG.
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxId=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CL BRENER;
RX MEDLINE=20209394; PubMed=10744707;
RA Di Noia J.M., D'Orso I., Sanchez D.O., Frasch A.C.;
RT "Aurich elements in the 3'-untranslated region of a new mucin-type
RT gene family of trypanosoma cruzi confers mRNA instability and
RT modulates translation efficiency.";
RL J. Biol. Chem. 275:10218-10227(2000).
DR EMBL: AF203096; AAF67333.1; -
SQ SEQUENCE 107 AA; 10811 MW; 7FCFE3307BD58420 CRC64;

Query Match 100.0%; Score 24; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLLVIA 6
| | | | |
Db 93 LLLVIA 98

RESULT 3

Q8XP09 PRELIMINARY; PRT; 110 AA.
AC Q8XP09;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-OCT-2000 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Probable transmembrane protein.
GN RSP1537 OR R504814.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Plasmid megaplasmid.
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxId=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Ganin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choisin N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigulier P., Thebaud P., Whalen M., Winkler P., Levy M.,
RA Welzenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646085; CAD18688.1; -
KW Plasmid; Complete proteome.
SQ SEQUENCE 110 AA; 12295 MW; 3F8A16A7F019E427 CRC64;

Query Match 100.0%; Score 24; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLLVIA 6
| | | | |
Db 72 LLLVIA 77

RESULT 4

Q9NIO2 PRELIMINARY; PRT; 128 AA.
AC Q9NIO2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Mucin-like protein.

GN SMUG.
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxId=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CL BRENER;
RX MEDLINE=20209394; PubMed=10744707;
RA Di Noia J.M., D'Orso I., Sanchez D.O., Frasch A.C.;
RT "Aurich elements in the 3'-untranslated region of a new mucin-type
RT gene family of trypanosoma cruzi confers mRNA instability and
RT modulates translation efficiency.";
RL J. Biol. Chem. 275:10218-10227(2000).
DR EMBL: AF203095; AAF67332.1; -
SQ SEQUENCE 128 AA; 12746 MW; 2DB356885D8E3715 CRC64;

Query Match 100.0%; Score 24; DB 5; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLLVIA 6
| | | | |
Db 114 LLLVIA 119

RESULT 5

Q9PCB9 PRELIMINARY; PRT; 159 AA.
AC Q9PCB9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein Xf0383.
GN Xf0383.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxId=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9ASC;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reineck F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bal G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bioness M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Gantier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnsels J.D., Junqueira M.L., Kemper E.L., Kitaajima J.P.,
RA Klieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Montelero-Vicorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nham J.A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,
RA Pelxoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Queglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE003890; AAF83193.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 159 AA; 17586 MW; 4666CA54D543D17 CRC64;

Query Match 100.0%; Score 24; DB 16; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 53 LLLVIA 58

RESULT 6
Q8TW28 PRELIMINARY; PRT; 173 AA.
AC Q8TW28;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Permease related to cation transporters.
GN MK0883.
GC Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Koonin E.V., Kozlovskiy S.A.,
Malykh A.G., Koonin E.V., Kozlovskiy S.A.,
"The complete genome of hyperthermophilic Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL: AE010378; AAM02096.1; -.
KW Complete proteome.
SQ SEQUENCE 173 AA; 17847 MW; PF7A3981C2A5B2E3 CRC64;

Query Match 100.0%; Score 24; DB 17; Length 173;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 93 LLLVIA 98

RESULT 7
Q9SIE7 PRELIMINARY; PRT; 183 AA.
AC Q9SIE7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Atg22170 protein.
GN ATG22170.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Beutlo M.-I., Town C.D.,
Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis

RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AC007168; AAD23623.1; -.
DR InterPro: IPR001024; Lipoxigenase_LH2.
DR Pfam: PF01477; Pfam: 1.
SQ SEQUENCE 183 AA; 20130 MW; B0322292368B92D CRC64;

Query Match 100.0%; Score 24; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 12 LLLVIA 17

RESULT 8
Q9MI04 PRELIMINARY; PRT; 193 AA.
AC Q9MI04;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit II (Fragment).
GN COX2.
OS Hypochytrium catenoides.
OC Mitochondrion.
OC Eukaryota; stramenopiles; Hyphochytriomycetes; Hyphochytriaceae;
OX Hypochytrium;
OC NCBI_TaxID=42384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC18719;
RA Hudspeeth D.S.S., Nadler S.A., Hudspeeth M.E.S.;
RT "A cytochrome c oxidase II molecular phylogeny of the
RT peronosporomycetes (oomycetes)."
RL Mycologia 92:674-684(2000).
DR EMBL: AF086701; AAF80243.1; -.
DR InterPro: IPR001505; Copper_CuA.
DR InterPro: IPR002429; Cyt_c-ox_2.
DR Pfam: PF00116; COX2; 1.
DR Pfam: PF02790; COX2_TM; 1.
DR PRINTS: PR01166; CYCOXIDASEII.
DR Prodom: PD000131; Copper_CuA; 1.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 193
SQ SEQUENCE 193 AA; 22017 MW; D28BD3E4A7A73B67 CRC64;

Query Match 100.0%; Score 24; DB 8; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
|||||
DB 65 LLLVIA 70

RESULT 9
Q8WET9 PRELIMINARY; PRT; 223 AA.
AC Q8WET9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COI.
OS Lyonsia hyalina.

```

OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Anomalodesmata; Pholadomyoidea;
OC Pandoroidea; Lyonsiidae; Lyonsia.
OX NCBI_TaxID=120442;
RN [1]
RP SEQUENCE FROM N.A.
RA Giribet G., Wheeler W.C.;
RT "On bivalve phylogeny: a high-level phylogeny of the mollusk class
RT Bivalvia based on a combined analysis of morphology and DNA sequence
RT data."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF120654; AAL55504.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 223
SQ SEQUENCE 223 AA: 24042 MW: 6758BFA6F2D1C725 CRC64;

Query Match 100.0%; Score 24; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 179 LLLVIA 184

RESULT 10
O44086 PRELIMINARY: PRT; 224 AA.
AC O44086;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ZK994.4 protein.
GN ZK994.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Watson L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC Davidson S., Wohlmann P.;
RT "The sequence of C. elegans cosmid ZK994."
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC Waterston R.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF022977; AAB88611.1; -.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Chem.
DR InterPro: IPR000372; LRR_Nterm.

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DR InterPro: IPR003592; LRR_out.
DR Pfam: PF00560; LRR; 3.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00370; LRR; 3.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
SQ SEQUENCE 224 AA: 25885 MW: A634CAE75770BC6A CRC64;

Query Match 100.0%; Score 24; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 6 LLLVIA 11

RESULT 11
O9YCB9 PRELIMINARY: PRT; 232 AA.
AC O9YCB9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein APE1337.
GN APE1337.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcales; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-K1;
RC MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Aikai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000061; BAA80329.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 232 AA: 24673 MW: E8CB8BF27691A0 CRC64;

Query Match 100.0%; Score 24; DB 17; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLLVIA 6
DB 82 LLLVIA 87

RESULT 12
O9ZBX3 PRELIMINARY: PRT; 239 AA.
AC O9ZBX3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Possible integral membrane protein.
GN SCO3959 OR SCD78.26.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-A3(2) / M145;

```

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajadream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RL coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL034355; CAA2231.1; -
 SO SEQUENCE 239 AA; 24760 MW; 73165C3F4F575A2 CRC64;

Query Match 100.0%; Score 24; DB 16; Length 239;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LLLVIA 6
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 29 LLLVIA 34

RESULT 13
 085820 PRELIMINARY; PRT; 248 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Polc.

GN Polc.
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 OS actinomycetemcomitans).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.

OX NCBI_TaxID=714;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-Y4.

RA Winston J.L., Szate S.A., Dyer D.W., McLaughlin R.E.;
 RT "Demonstration of a polyamine requirement for growth of Actinobacillus
 RT actinomycetemcomitans, and identification of the putative polyamine
 RT transport operon.";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM.
 CC -1- FUNCTION: RESPONSIBLE FOR THE TRANSLLOCATION OF THE SUBSTRATE ACROSS
 CC THE MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.

CC EMBL: AF077856; AAC27497.1; -
 CC InterPro: IPR000515; BPD_transp.

DR Pfam: PF00528; BPD_transp. 1.
 DR PROSITE: PS00402; BPD_TRANSP_INN_MEMBR. 1.

KW Transmembrane; Transport.
 KW SEQUENCE 248 AA; 27390 MW; 3f641c8a87356607 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
 |||||

DB 232 LLLVIA 237

RESULT 14

P72696 PRELIMINARY; PRT; 281 AA.

AC P72696; 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Created)

QY 1 LLLVIA 6
 |||||

DB 232 LLLVIA 237

RESULT 14

P72696 PRELIMINARY; PRT; 281 AA.

AC P72696; 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein slr0241.
 GN SLR0241.
 OS Synechocystis sp. (Strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyaajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D90900; BAA16703.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 281 AA; 31695 MW; 08CA1C1D6D5DA1B CRC64;

Query Match 100.0%; Score 24; DB 16; Length 281;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
 |||||
 DB 264 LLLVIA 269

RESULT 15

Q8ZDP9 PRELIMINARY; PRT; 295 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative membrane protein.
 DE YPO2507.
 GN Yersinia pestis.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.

OX NCBI_TaxID=632;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CO-92 / BIOVAR ORIENTALIS;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Fellwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
 RT Nature 413:523-527(2001).
 RL EMBL: AJ414152; GAC91312.1; -
 DR InterPro: IPR000620; DUF6.
 DR Pfam: PF00892; DUF6. 1.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 295 AA; 30755 MW; 1174738653C02B7 CRC64;

Query Match 100.0%; Score 24; DB 16; Length 295;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLVIA 6
 |||||

DB 17 LLLVIA 22

Mon Jan 6 15:08:51 2003

us-09-543-188a-13.rspc

Page 6

Search completed: January 3, 2003, 15:31:59
Job time : 21.3182 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:21:45 : Search time 26.5909 Seconds
(without alignments)
30.067 Million cell updates/sec

Title: US-09-543-188a-21

Perfect score: 34
Sequence: 1 IQWTF 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	6	23	AAU11844
2	32	94.1	49	22	AAE10210
3	32	94.1	79	21	AA606438
4	32	94.1	79	21	AA624460
5	32	94.1	79	21	AA635187
6	32	94.1	79	21	AA635298
7	32	94.1	88	21	AA606437
8	32	94.1	88	21	AA624459
9	32	94.1	88	21	AA635186
10	32	94.1	88	21	AA635297

11	32	94.1	101	23	AB660097
12	32	94.1	110	23	AB660099
13	32	94.1	126	21	AA635185
14	31	91.2	2243	22	AB629035
15	31	91.2	2478	22	AB630281
16	30	88.2	51	21	AA603171
17	30	88.2	51	22	AB114713
18	30	88.2	52	23	ABP07377
19	30	88.2	70	20	AA114458
20	30	88.2	74	21	AA617988
21	30	88.2	98	22	AAU60587
22	30	88.2	122	21	AA617987
23	30	88.2	123	21	AA617986
24	30	88.2	305	23	ABP27371
25	30	88.2	305	23	AAU77623
26	30	88.2	603	22	AB621614
27	30	88.2	739	22	ABG03417
28	30	88.2	739	22	ABG09732
29	30	88.2	739	22	ABG12286
30	29	85.3	24	7	AA60356
31	29	85.3	115	22	AA65123
32	29	85.3	179	22	AA687351
33	29	85.3	179	23	AB665354
34	29	85.3	185	22	AA663958
35	29	85.3	261	22	AB687428
36	29	85.3	352	22	AAU31812
37	29	85.3	371	22	AB65431
38	29	85.3	391	19	AAW30680
39	29	85.3	391	19	AAW60255
40	29	85.3	391	19	AAW57324
41	29	85.3	391	20	AAV26166
42	29	85.3	391	22	AA674887
43	29	85.3	433	20	AAU03770
44	29	85.3	433	21	AAV90622
45	29	85.3	433	21	AAV90656

ALIGNMENTS

RESULT 1	AAU11844
ID	AAU11844 standard; peptide; 6 AA.
XX	AAU11844:
AC	AAU11844:
DT	26-MAR-2002 (first entry)
XX	
DE	Peptide ligand for Prion protein, PrP, #19.
XX	
KW	Prion protein; PrP; ligand; octapeptide motif; scrapie;
KW	Prion-associated disease; Creutzfeldt-Jakob disease;
KW	Gerstmann-Strausler-Scheinker disease; fatal familial insomnia;
KW	Feline spongiform encephalopathy; bovine spongiform encephalopathy;
KW	transmissible mink encephalopathy; exotic ungulate encephalopathy;
KW	chronic wasting disease.
XX	
OS	Synthetic.
XX	
PN	WO200177687-A2.
XX	
PD	18-OCT-2001.
XX	
PF	05-APR-2001; 2001MO-US11150.
XX	
PR	05-APR-2000; 2000US-0543188.
XX	
PA	(VITE-) VI TECHNOLOGIES INC.
XX	
PI	Hammond DJ, Wiltshire VR, Cardonell R, Shen H;
XX	
DR	WPI; 2002-061944/08.
XX	

Human DTRP polype
Human DTRP polype
Zea mays protein f
Novel human diago
Novel human diago
Human secreted pro
Human nervous syst
Human OREX protein
Human secreted pro
Arabidopsis thalia
Propionibacterium
Arabidopsis thalia
Arabidopsis thalia
Streptococcus poly
S. agalactiae extr
Novel human diago
Novel human diago
Novel human diago
Novel human diago
Sequence of human
Propionibacterium
Human gene 10 enco
Human albumin fusi
Human prostate can
Human gene 10 enco
Novel human secret
Drosophila melanog
Glycerol-3-phospha
Klebsiella pneumon
Cytosolic glycerol
Saccharomyces cere
Human G-protein co
Human G protein-co
Human mutant G pro

PT New ligands for prion proteins, useful for detection or removal or
PT prions and for treating prion-associated diseases, recognize a specific
PT octapeptide motif -

PS Claim 16; Page 34; 47pp; English.

XX The invention relates to a ligand of less than 6 kD that binds to a
CC polypeptide containing the sequence GLYTYGLYGLNPROHISGLYGLY (A) or an
CC analogue that is the retro-inverso isomer of (A). The sequence A is
CC an octapeptide motif from the prion protein (PrP). The ligands are
CC identified by binding assays with the peptide (A) or peptides containing
CC (A). The ligands are used for detecting prion proteins (or prions) in
CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jakob diseases (in
CC latrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strausler-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is a ligand of the invention.

Sequence 6 AA:

Query Match 100.0%; Score 34; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWIIF 6
| | | | |
Db 1 IQIWIIF 6

RESULT 2

AAE10210
ID AAE10210 standard; peptide; 49 AA.

AC AAE10210;

DT 29-NOV-2001 (first entry)

DE Human bone marrow derived contig peptide, SEQ ID NO: 75.

KW Human; bone marrow; cytokine; cell proliferation; cell differentiation;
KW stem cell growth; haematopoiesis regulation; immunoregulatory; anaemia;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW Infection; HIV; malaria; fungal; cancer; autoimmune disorder; arthritis;
KW Crohn's disease; Inflammatory bowel disease; leukaemia; gene therapy.

XX Homo sapiens.

WO200166558-A1.

13-SEP-2001.

07-MAR-2001; 2001WO-US07774.

07-MAR-2000; 2000US-0519705.

19-MAY-2000; 2000US-0574454.

14-JUL-2000; 2000US-0616847.

30-NOV-2000; 2000US-0250583.

(HYSE-) HYSBQ INC.

PI Ford JE, Boyle BJ, Tang YT, Liu C, Zhou P, Asundi V, Zhang J;
PI Drmanac RT;

XX WPI; 2001-565565/63.

DR N-PSDB; AAD17391.

PT Isolated polynucleotide encoding bone marrow derived polypeptides
PT useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis,
PT Crohn's disease, and inflammatory bowel disease

PS Claim 10; Page 113; 169pp; English.

XX The invention relates to novel human bone marrow polynucleotides and
CC polypeptides. The polypeptides of the invention may exhibit various
CC activities e.g. cytokine and cell proliferation/differentiation,
CC stem cell growth, haematopoiesis regulation and immune stimulation/
CC suppression. The polynucleotides and polypeptides of the invention may
CC be used to detect bone marrow cells, for treating, e.g., Parkinson's
CC disease, Alzheimer's disease, anaemia, amyotrophic lateral sclerosis,
CC infections such as HIV, malaria and fungal infections, cancer, autoimmune
CC disorders, arthritis, Crohn's disease, inflammatory bowel disease, and
CC leukaemia. The polynucleotide may also be used as markers for tissues in
CC which the corresponding protein is preferentially expressed; as molecular
CC weight markers and as probes to hybridise and discover novel, related DNA
CC sequences. The polypeptide may be used in assays to determine biological
CC activity, to raise antibodies or illicit an immune response and as a
CC reagent in assays. The present sequence is a human bone marrow derived
CC contig peptide of the invention.

Sequence 49 AA:

Query Match 94.1%; Score 32; DB 22; Length 49;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWIIF 6
: | | | : |
Db 6 VQIWIIF 11

RESULT 3

AAG06438
ID AAG06438 standard; Protein; 79 AA.

AC AAG06438;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 3211.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126264.

29-MAR-1999; 99US-0126785.

01-APR-1999; 99US-0127462.

06-APR-1999; 99US-0128234.

08-APR-1999; 99US-0128714.

16-APR-1999; 99US-0129845.

19-APR-1999; 99US-0130077.

21-APR-1999; 99US-0130449.

23-APR-1999; 99US-0130510.

23-APR-1999; 99US-0130891.

28-APR-1999; 99US-0131449.

30-APR-1999; 99US-0132048.

30-APR-1999; 99US-01332407.

04-MAY-1999; 99US-01332484.

05-MAY-1999; 99US-01332485.

06-MAY-1999; 99US-01332486.

06-MAY-1999; 99US-01332487.

PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0138119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139750.
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Best Local Similarity 83.3%; Pred. No. 1e+02;
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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PD 06-SEP-2000.
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Best Local Similarity 83.3%; Pred. No. 1e+02;
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DT 18-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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OS Zea mays subsp. mays.
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Query Match 94.1%; Score 32; DB 21; Length 79;
Best Local Similarity 83.3%; Pred. No. 1e+02;
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AC AAG35298;

DT 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 43098.

XX Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence; corn.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;	
KW termination sequence.	
XX	
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XX	
PN EP1033405-A2.	
XX	
PD 06-SEP-2000.	
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XX 17-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
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XX AAG35186;

XX 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 42947.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence; corn.
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Query Match 94.1%; Score 32; DB 21; Length 88;
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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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ID AAG35297 standard; Protein; 88 AA.

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XX 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 43097.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.

XX EPI033405-A2.

XX 06-SEP-2000.

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PR	13-OCT-1999;	990US-0159295;
PR	14-OCT-1999;	990US-0159329;
PR	14-OCT-1999;	990US-0159330;
PR	14-OCT-1999;	990US-0159331;
PR	14-OCT-1999;	990US-0159637;
PR	14-OCT-1999;	990US-0159638;
PR	18-OCT-1999;	990US-0159584;
PR	21-OCT-1999;	990US-0160741;
PR	21-OCT-1999;	990US-0160767;
PR	21-OCT-1999;	990US-0160768;
PR	21-OCT-1999;	990US-0160770;
PR	21-OCT-1999;	990US-0160814;
PR	21-OCT-1999;	990US-0160815;
PR	22-OCT-1999;	990US-0160980;
PR	22-OCT-1999;	990US-0160981;
PR	22-OCT-1999;	990US-0160989;
PR	25-OCT-1999;	990US-0161404;
PR	25-OCT-1999;	990US-0161405;
PR	25-OCT-1999;	990US-0161406;
PR	26-OCT-1999;	990US-0161359;
PR	26-OCT-1999;	990US-0161360;
PR	26-OCT-1999;	990US-0161361;
PR	28-OCT-1999;	990US-0161920;
PR	28-OCT-1999;	990US-0161992;
PR	28-OCT-1999;	990US-0161993;
PR	29-OCT-1999;	990US-0162142;

Query Match	94.1%;	Score 32;	DB 21;	Length 88;
Best Local Similarity	83.38;	Pred. No. 11e+02;		
Matches 5;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 IQIWI 6			
	:			
Db	27 IQIWI 32			
RESULT 11				
	360097			
	ABG60097 standard; Protein; 101 AA.			
XX	ABG60097;			
AC				
XX				
DT	30-JUL-2002 (first entry)			
XX				
DE	Human DITHP polypeptide #155.			
XX				
XX	Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;			
KW	cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;			
KW	inflammatory disorder; viral infection; bacterial infection; seizure;			
KW	fungal infection; parasitic infections; developmental disorder; breast;			
KW	endocrine disorder; metabolic disorder; neurological disorder; cervix;			
KW	gastrointestinal disorder; transport disorder; gene therapy; kidney;			
KW	adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;			
KW	thymus.			
XX				
OS	Homo sapiens.			
XX				
PN	W0200220754-A2.			
XX				
PD	14-MAR-2002.			
XX				
PF	29-AUG-2001; 2001WO-US27127.			

XX	05-SEP-2000.	2000US-229747P.
PR	05-SEP-2000.	2000US-229748P.
PR	05-SEP-2000.	2000US-229749P.
PR	05-SEP-2000.	2000US-229750P.
PR	05-SEP-2000.	2000US-229751P.
PR	05-SEP-2000.	2000US-230563P.
PR	06-SEP-2000.	2000US-230505P.
PR	06-SEP-2000.	2000US-230514P.
PR	06-SEP-2000.	2000US-230515P.
PR	06-SEP-2000.	2000US-230517P.
PR	06-SEP-2000.	2000US-230518P.
PR	06-SEP-2000.	2000US-230519P.
PR	06-SEP-2000.	2000US-230595P.
PR	06-SEP-2000.	2000US-230597P.
PR	06-SEP-2000.	2000US-230598P.
PR	06-SEP-2000.	2000US-230599P.
PR	06-SEP-2000.	2000US-230610P.
PR	06-SEP-2000.	2000US-230658P.
PR	06-SEP-2000.	2000US-230968P.
PR	07-SEP-2000.	2000US-230951P.
PR	07-SEP-2000.	2000US-231163P.
PR	07-SEP-2000.	2000US-231167P.

WPI: 2002-383054/41.
N-PSDB; ABK71688.

An isolated polynucleotide useful in diagnostics and therapeutics -
Claim 29; Page 621; 686pp; English.

CC The invention relates to human diagnostic and therapeutic (dihp)
CC polypeptides and their associated polypeptides (DTRP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
CC A6539943-AB60220 represent human DTRP polypeptides of the invention.

Seq	Sequence	101 AA;	94.1%;	Score 32;	DB 23;	Length 101;
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	Best Local Similarity	83.3%;		Pred. No. 1.3e+02;		
	Matches	5;	Conservative	1;	Mismatches	0;
					Indels	0;
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QY	1 IQIWIIF 6					
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RESULT 12						
ABG60099						
ID	ABG60099	standard;	Protein;	110 AA.		
XX						
AC	ABG60099;					
XX						

30-JUL-2002 (first entry)
Human DTRHP polypeptide #157.
Human; DTRHP, diagnostic and therapeutic polypeptide; bone; testis; skin;
cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
inflammatory disorder; viral infection; bacterial infection; seizure;
fungal infection; parasitic infections; developmental disorder; breast;
endocrine disorder; metabolic disorder; neurological disorder; cervix;
gastrointestinal disorder; transport disorder; gene therapy; kidney;
adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
thymus.
Homo sapiens.
WO200220754-A2.
14-MAR-2002.
29-AUG-2001; 2001WO-US27127.
05-SEP-2000; 2000US-229747P.
05-SEP-2000; 2000US-228748P.
05-SEP-2000; 2000US-229749P.
05-SEP-2000; 2000US-229750P.
05-SEP-2000; 2000US-229751P.
05-SEP-2000; 2000US-230583P.
06-SEP-2000; 2000US-230505P.
06-SEP-2000; 2000US-230514P.
06-SEP-2000; 2000US-230515P.
06-SEP-2000; 2000US-230517P.
06-SEP-2000; 2000US-230518P.
06-SEP-2000; 2000US-230519P.
06-SEP-2000; 2000US-230595P.
06-SEP-2000; 2000US-230597P.
06-SEP-2000; 2000US-230598P.
06-SEP-2000; 2000US-230599P.
06-SEP-2000; 2000US-230610P.
06-SEP-2000; 2000US-230865P.
06-SEP-2000; 2000US-230988P.
07-SEP-2000; 2000US-230951P.
07-SEP-2000; 2000US-231163P.
07-SEP-2000; 2000US-231167P.
(INCY-) INCYTE GENOMICS INC.
Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL,
Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
Moriyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A,
Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
WPL: 2002-383054/41.
N-PSDB; ABR71690.
An isolated polynucleotide useful in diagnostics and therapeutics -
Claim 29: Page 622; 686bp; English.
The invention relates to human diagnostic and therapeutic (dtrhp)
polynucleotides and their associated polypeptides (DTRHP polypeptides).
The sequences of the invention are used in the treatment and diagnosis of
cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
(e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
psoriasis, osteoporosis), viral infections, bacterial infections, fungal
infections, parasitic infections, developmental disorders (e.g. anemia,
epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
(e.g. obesity, diabetes), neurological disorders (e.g. stroke,
amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
disorders (e.g. ulcerative colitis, lysinuria) and transport disorders

(e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
CC AAG5943-ABG60220 represent human DTRHP polypeptides of the invention.
SQ Sequence 110 AA:
Query Match 94.1%; Score 32; DB 23; Length 110;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IQIWIIF 6
DB 57 IQIWIIF 62
RESULT 13
AAG35185
ID AAG35185 standard; Protein; 126 AA.
AC AAG35185;
XX 18-OCT-2000 (first entry)
DE Zea mays protein fragment SEQ ID NO: 42946.
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
OS Zea mays subsp. mays.
PN EP1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 07-MAY-1999; 99US-0132863.
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PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
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 PR 02-AUG-1999; 99US-0146386.
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 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
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 PR 18-OCT-1999; 99US-0159584.
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 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
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 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
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 PR 22-OCT-1999; 99US-0160989.
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 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161927.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 94.1%; Score 32; DB 21; Length 126;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
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Db 65 IQIWF 70

RESULT 14
ABG29035
ID ABG29035 standard; Protein; 2243 AA.

XX ABG29035;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #29026.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN MO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS93222.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 20; SEQ ID No 59394; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2243 AA;

Query Match 91.2%; Score 31; DB 22; Length 2243;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
||||:|

Db 328 IQIWF 333

RESULT 15
ABG30281
ID ABG30281 standard; Protein; 2478 AA.

XX ABG30281;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #30272.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN MO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS94468.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 20; SEQ ID No 60640; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2478 AA;

Query Match 91.2%; Score 31; DB 22; Length 2478;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Mon Jan 6 15:08:52 2003

us-09-543-188a-21.rag

Page 18

Db 563 IQIWF 568

Search completed: January 3, 2003, 15:28:40
Job time : 28.5909 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:00 : Search time 9.95455 seconds
(without alignments)
57.944 Million cell updates/sec

Title: US-09-543-188a-21

Perfect score: 34

Sequence: 1 IQIWF 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	97.1	282	2 C58933	ribosomal protein
2	33	97.1	285	2 T24123	hypothetical prote
3	33	97.1	360	2 G83831	spore germination
4	32	94.1	86	2 F85354	small nuclear ribo
5	32	94.1	88	2 A84568	probable small nuc
6	32	94.1	495	2 T12401	NADH2 dehydrogenas
7	31	91.2	394	2 E81286	probable polysacch
8	30	88.2	218	1 R3NT3	ribosomal protein
9	30	88.2	218	1 R3SP3	ribosomal protein
10	30	88.2	220	2 S78395	ribosomal protein
11	30	88.2	229	2 E70340	glutaredoxin-like
12	30	88.2	240	2 S59085	ribosomal protein
13	30	88.2	309	2 T34080	hypothetical prote
14	30	88.2	347	2 T50963	related to cell pr
15	30	88.2	488	2 C59240	type II site-speci
16	29	85.3	144	2 G84935	hypothetical prote
17	29	85.3	217	1 R3LV3	ribosomal protein
18	29	85.3	222	2 B95207	aquaporin [impor
19	29	85.3	222	2 B98072	aquaporin Z, water
20	29	85.3	224	2 S58590	ribosomal protein
21	29	85.3	231	2 T07358	ribosomal protein
22	29	85.3	239	1 R3RZ3	ribosomal protein
23	29	85.3	240	2 S77496	ribosomal protein
24	29	85.3	243	2 E97593	30S ribosomal prot
25	29	85.3	243	2 A82815	30S ribosomal prot
26	29	85.3	244	2 T11241	Sect-independent t
27	29	85.3	252	2 B41839	ribosomal protein
28	29	85.3	327	2 S76951	hypothetical prote
29	29	85.3	348	2 D70195	hypothetical prote

30	29	85.3	373	2 P00042	actavin - fruit fl
31	29	85.3	391	2 S40059	glycerol-3-phospha
32	29	85.3	583	2 T02382	hypothetical prote
33	29	85.3	720	2 T02361	hypothetical prote
34	29	85.3	920	1 P4NCP	H+-exporting Atpas
35	29	85.3	978	1 RCBY13	regulatory protein
36	28	82.4	71	2 T51537	hypothetical prote
37	28	82.4	90	2 T27041	hypothetical prote
38	28	82.4	92	2 A32127	small nuclear ribo
39	28	82.4	122	2 A31090	hypothetical 14k p
40	28	82.4	122	2 AC1808	ATP synthase chain
41	28	82.4	205	2 PC2191	ribosomal protein
42	28	82.4	219	1 R3KT3	ribosomal protein
43	28	82.4	227	2 T11185	H+-transporting tw
44	28	82.4	227	2 F90622	ATP synthase F0 ch
45	28	82.4	228	2 G83115	30S ribosomal prot

ALIGNMENTS

```
RESULT 1
C58933
ribosomal protein S3 - Cyanidioschyzon merolae mitochondrion
C:Species: mitochondrion Cyanidioschyzon merolae
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 05-Nov-1999
C:Accession: C58933
R:Ohta, N.; Sato, N.; Kuroiwa, T.
Nucleic Acids Res. 26, 5190-5198, 1998
A:Title: Structure and organization of the mitochondrial genome of the unicellular re
A:Reference number: A58930; MUID:99030526; PMID:9801318
A:Accession: C58933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <ARN>
A:Cross-references: GB:D89861; NID:g4115781; PIDN:BAA36537.1; PID:d1037523; PID:g4115
C:Genetics:
A:Gene: rps3
A:Genome: mitochondrion
C:Keywords: mitochondrion

Query Match
Best local Similarity 97.1%; Score 33; DB 2; Length 282;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
Db 275 IQIWF 280

RESULT 2
T24123
hypothetical protein R10D12.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T24123
R:Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19842
A:Accession: T24123
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-285 <MIT>
A:Cross-references: EMBL:Z81109; PIDN:CAB03254.1; GSPDB:GN00023; CESP:R10D12.11
C:Genetics:
A:Experimental source: clone R10D12
A:Gene: CESP:R10D12.11
A:Map position: 5
A:Introns: 51/2; 165/3; 240/3
C:Superfamily: Caenorhabditis hypothetical protein C4967.2

Query Match
Best local Similarity 97.1%; Score 33; DB 2; Length 285;
```

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IQIWF 6
:|||||
Db 48 VOIWF 53

RESULT 3

spore germination protein BH1455 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G83831
R:Takeml, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <STO>
A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA805174.1; GSPDB:GN00
A:Experimental source: strain C-125
A:Gene: BH1455

Query Match 97.1%; Score 32; DB 2; Length 360;
Best Local Similarity 83.3%; Pred. No. 59;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
:|||||
Db 109 IQIWF 114

RESULT 4

small nuclear ribonucleoprotein homolog [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: F85354
R:anonymus, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85354
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <STO>
A:Cross-references: GB:NC_001268; NID:g7269933; PIDN:CAB81026.1; GSPDB:GN00140
A:Genetics:

A:Map position: 4
A:Gene: AT4G30330
Query Match 94.1%; Score 32; DB 2; Length 86;
Best Local Similarity 83.3%; Pred. No. 23;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
:|||||
Db 27 IQIWF 32

RESULT 5

probable small nuclear ribonucleoprotein E [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84568
R:Rilo, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Mofeit, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84568
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <STO>
A:Cross-references: GB:AE002093; NID:g4185140; PIDN:AAD08943.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g18740
A:Map position: 2

Query Match 94.1%; Score 32; DB 2; Length 88;
Best Local Similarity 83.3%; Pred. No. 23;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
:|||||
Db 27 IQIWF 32

RESULT 6

MDH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - *Sarcophyton glaucum* mitochond

C:Species: *Sarcophyton glaucum*
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Jun-2002
C:Accession: T12401
R:Beaton, M.J.; Roger, A.J.; Cavallier-Smith, T.

J. Mol. Evol. 47, 697-708, 1998

A:Title: Sequence analysis of the mitochondrial genome of *Sarcophyton glaucum*: Conser
A:Reference number: Z17505; MUID:99065763; PMID:9847412

A:Accession: T12401
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-495 <BEA>

A:Cross-references: EMBL:AF064823; NID:g4091912; PID:g4091917; PIDN:AAC39651.1

C:Genetics:

A:Genome: mitochondrion

A:Note: ND4

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: membrane-associated complex; mitochondrion; NMD; oxidative phosphorylation

Query Match 94.1%; Score 32; DB 2; Length 495;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
:|||||
Db 219 IQIWF 224

RESULT 7

probable polysaccharide modification protein Cj1413c [imported] - *Campylobacter jejuni*

C:Species: *Campylobacter jejuni*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: E81286
R:Parthall, J.; Wren, B.W.; Mungall, K.; Kelley, J.M.; Churcher, C.; Basham, D.; Chil
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanvliet, A.; Whitehead, S.; Bar
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: E81286
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <PAR>

A:Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73837.1; PID:g696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1413c
C:Superfamily: kpsd protein

Query Match 91.2%; Score 31; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IQIWF 6
|:||||
Db 105 IEIWF 110

RESULT 8
R3NT3

ribosomal protein S3, chloroplast - common tobacco chloroplast
C:Species: chloroplast Nicotiana tabacum (common tobacco)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 30-Jan-1998
C:Accession: A02702; E25943

R: Sugita, M.
submitted to the EMBL Data Library, August 1986
A:Reference number: A00149

A:Accession: A02702
A:Molecule type: DNA
A:Residues: 1-218 <SUG>

A:Experimental source: cv. Bright yellow 4
Shinozaki, K.; Ohme, M.; Tanaka, M.; Makasugi, T.; Hayashida, N.; Matsubayashi, T.; Zä
eno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tondoh, N.; Sh

EMBO J. 5, 2043-2049, 1986
A>Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene or
A:Reference number: A38013

A:Contents: annotation; gene organization, sites, features
R: Tanaka, M.; Makasugi, T.; Sugita, T.; Shinozaki, K.; Sugita, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 6030-6034, 1986

A>Title: Genes for the eight ribosomal proteins are clustered on the chloroplast genome
A:Reference number: A94118; M01D:86287388; PMID:3016736

A:Accession: E25943
A:Molecule type: DNA
A:Residues: 1-218 <TRAN>

C:Genetics:
A:Gene: rps3

A:Genome: chloroplast
C:Superfamily: Escherichia coli ribosomal protein S3
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 88.2%; Score 30; DB 1; Length 218;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
|:||||
Db 209 IKIWF 214

●●●●●
ULF 9
P3

ribosomal protein S3, chloroplast - spinach chloroplast
C:Species: chloroplast Spinacia oleracea (spinach)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C:Accession: S01978

R: Zhou, D.X.; Quigley, F.; Massenet, O.; Mache, R.
Mol. Gen. Genet. 216, 439-445, 1989
A>Title: Cotranscription of the S10- and spc-like operons in spinach chloroplasts and id

A:Reference number: S01976; M01D:89313684; PMID:2747623
A:Accession: S01978
A:Molecule type: DNA
A:Residues: 1-218 <ZHO>

A:Cross-references: EMBL:X13336; NID:g12307; PIDN:CAA31745.1; PID:g12310
C:Genetics:
A:Gene: rps3

A:Genome: chloroplast
C:Superfamily: Escherichia coli ribosomal protein S3
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 88.2%; Score 30; DB 1; Length 218;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6

Db 209 IKIWF 214
|:||||

RESULT 10
S78395

ribosomal protein S3, plastid - beechdrops plastid
C:Species: plastid Epifagus virginiana (beechdrops)
C>Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Aug-1999
C:Accession: S78395

R: Wolfe, K.H.; Morden, C.W.; Ems, S.C.; Palmer, J.D.
J. Mol. Evol. 35, 304-317, 1992
A>Title: Rapid evolution of the plastid translational apparatus in a nonphotosynthetic

A:Reference number: S78378; M01D:93021155; PMID:1404416
A:Accession: S78395
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-220 <MOL>

A:Cross-references: EMBL:M81884; NID:g336917; PIDN:AA65864.1; PID:g336936
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C:Genetics:

A:Gene: rps3
A:Genome: plastid
C:Superfamily: Escherichia coli ribosomal protein S3
C:Keywords: plastid; protein biosynthesis; ribosome

Query Match 88.2%; Score 30; DB 2; Length 220;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
|:||||
Db 211 IKIWF 216

RESULT 11
E70340

glutaredoxin-like protein - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: E70340

R: Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; M01D:98196666; PMID:9537320
A:Accession: E70340
A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-229 <AOE>

A:Cross-references: GB:AE000690; M01D:g2983100; PIDN:AA06709.1; PID:g2983104; GB:AE00
A:Experimental source: strain VF5
C:Genetics:
A:Gene: gua

Query Match 88.2%; Score 30; DB 2; Length 229;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
|:||||
Db 138 IEIWF 143

RESULT 12
S59085

ribosomal protein S3, mitochondrial - red alga (Chondrus crispus) mitochondrion
C:Species: mitochondrial Chondrus crispus (carrageen)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jul-2000
C:Accession: S59085

R: Leblanc, C.; Boyen, C.; Richard, O.; Bonnard, G.; Grienenberger, J.M.; Kloareg, B.
J. Mol. Biol. 250, 484-495, 1995
A>Title: Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus

Query Match 88.2%; Score 30; DB 2; Length 229;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

A:Reference number: S59078; MUID:95341681; PMID:7616569
 A:Accession: S59085
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-240 <LEB>
 A:Cross-references: EMBL:247547; NID:g1019057; PIDN:CA87601.1; PID:g1334481
 A:Experimental source: female gametophytes
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 C:Genetics:
 A:Gene: rps3
 A:Genome: mitochondrion
 A:Genetic code: SGC3
 C:Function:
 A:Pathway: protein biosynthesis
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 88.2%; Score 30; DB 2; Length 240;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 QIWIIF 6
 :|:|:
 Db 220 VQVWLF 225

RESULT 13
 T34080
 hypothetical protein C02F12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T34080
 R:Miller, N.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C02F12.
 A:Reference number: Z21473
 A:Accession: T34080
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-309 <MIL>
 A:Cross-references: EMBL:U41545; PIDN:AAA83189.1; CESP:C02F12.1
 C:Genetics:
 A:Gene: CESP:C02F12.1
 A:introns: 23/3; 58/3; 83/3; 140/3; 178/3; 257/3; 285/3

Query Match 88.2%; Score 30; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 QIWIIF 6
 :|:|:
 Db 270 QIWIIF 274

RESULT 14
 T50963
 related to cell protein precursor [imported] - Neurospora crassa
 N:Alternate names: protein B24P7.180
 C:Species: Neurospora crassa
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
 C:Accession: T50963
 R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, July 2000
 A:Reference number: Z25286
 A:Accession: T50963
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <SCH>
 A:Cross-references: EMBL:AL389890; GSPDB:GNO0116; NCSP:B24P7.180
 C:Experimental source: BAC clone B24P7; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B24P7.180
 A:Map position: 6

Query Match 88.2%; Score 30; DB 2; Length 347;
 Best Local Similarity 50.0%; Pred. No. 2.1e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIWIIF 6
 :|:|:
 Db 206 VQVWLF 211

RESULT 15
 C59240
 type II site-specific deoxyribonuclease (EC 3.1.21.4) HgaI - Haemophilus paragaillinar
 C:Species: Haemophilus paragaillinarum
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 20-Jun-2000
 C:Accession: C59240
 R:Sugisaki, H.
 Bull. Inst. Chem. Res. Kyoto Univ. 71, 338-342, 1993
 A:Title: Nucleotide sequence of the gene of HgaI restriction endonuclease.
 A:Reference number: A59239
 A:Accession: C59240
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-488 <SUG>
 A:Cross-references: GB:D17388; NID:g393310; PIDN:BAA04208.1; PID:g393313
 A:Experimental source: strain NCTC 3438
 C:Superfamily: Haemophilus paragaillinarum type II site-specific deoxyribonuclease Hga
 C:Keywords: hydrolase

Query Match 88.2%; Score 30; DB 2; Length 488;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QIWIIF 6
 :|:|:
 Db 11 QIWIIF 15

Search completed: January 3, 2003, 15:33:18
 Job time : 10.9545 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:22:10 : Search time 5.18182 Seconds
(without alignments)
48.025 Million cell updates/sec

Title: US-09-543-188A-21

Sequence: 34
1 IQIWI 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	94.1	224	1 MTGA_ACICA	Q24849 acinetobact
2	30	88.2	218	1 RR3_ARATH	P56798 arabidopsi
3	30	88.2	218	1 RR3_SPTOL	F09595 spinachia ol
4	30	88.2	218	1 RR3_TOBAC	F06357 nicotiana t
5	30	88.2	220	1 RR3_ERIYI	P30055 epifagus vi
6	30	88.2	240	1 RT03_CHOCR	P48938 chondrus cr
7	30	88.2	277	1 YL11_CAEBL	Q11098 caenorhabdi
8	30	88.2	484	1 T2G1_HAEGA	P43418 haemophilus
9	29	85.3	144	1 Y052_BUCAT	F57160 buchnera ap
10	29	85.3	213	1 RR3_MESVI	Q6muu2 mesostigma
11	29	85.3	217	1 RR3_MARPO	P06356 marchantia
12	29	85.3	224	1 RR3_MAIZE	P06586 zea mays (m
13	29	85.3	231	1 RR3_CHLVU	P56365 chlorella v
14	29	85.3	239	1 RR3_ORYSA	F12146 oryza sativ
15	29	85.3	239	1 RS3_SYNY3	P73314 synchocyst
16	29	85.3	252	1 RS3_ASTYP	Q50267 aster yello
17	29	85.3	252	1 RS3_PHY52	Q66098 phytoplasma
18	29	85.3	324	1 CP21_HORVU	P55747 hordeum vul
19	29	85.3	391	1 GPDI_YEAST	Q00055 saccharomyc
20	29	85.3	433	1 GP22_HUMAN	Q09680 homo sapien
21	29	85.3	430	1 PMAI_NEUCR	P07038 neurospora
22	29	85.3	978	1 STR3_YEAST	P06701 saccharomyc
23	28	82.4	92	1 RUXE_HUMAN	P08578 homo sapien
24	28	82.4	122	1 ATPZ_ANASP	P14403 anabaena sp
25	28	82.4	205	1 RS3_BUCAR	P46172 buchnera ap
26	28	82.4	216	1 RR3_GUITH	Q46900 guillardia
27	28	82.4	219	1 RR3_CYAPA	P23401 cyanophora
28	28	82.4	232	1 RS3_ECOLI	P02352 escherichia
29	28	82.4	233	1 RS3_BUCAT	P57585 buchnera ap
30	28	82.4	234	1 RS3_ACTAC	P55827 actinobacill
31	28	82.4	234	1 RS3_HAEIN	P43372 haemophilus
32	28	82.4	234	1 RS3_HELPJ	Q93199 helicobacte
33	28	82.4	234	1 RS3_HELPY	P56010 helicobacte

34	28	82.4	243	1 RS3_SYNP6	O24695 synchococc
35	28	82.4	248	1 RS3_ACHSP	P41118 achloleplasm
36	28	82.4	251	1 RS3_PHY51	O66095 phytoplasma
37	28	82.4	270	1 VSP1_ARATH	O49195 arabidopsi
38	28	82.4	313	1 FIXB_ECOLI	P31574 escherichia
39	28	82.4	326	1 YE09_SYNY3	P73594 synchocyst
40	28	82.4	340	1 CTR1_PIG	Q95002 sus scrofa
41	28	82.4	374	1 YFRB_SPTCI	P27712 spiriplasma
42	28	82.4	509	1 CCB5_MARPO	P36180 marchantia
43	28	82.4	515	1 NCAP_P13H4	P06159 human para
44	28	82.4	551	1 NCAP_P13H4	P17241 human para
45	28	82.4	712	1 RR3_CHLRE	Q08365 chlamydomon

ALIGNMENTS

RESULT 1

ID	MTGA_ACICA	STANDARD:	PRT:	224 AA.
AC	Q24849:			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.4.2.-) (Monofunctional tase).			
GN	MTGA.			
OS	Acinetobacter calcoaceticus.			
OC	Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;			
OC	Acinetobacter.			
OX	NCBI_TaxID=471;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BD413 / ADP1;			
RX	MEDLINE=95400495; PubMed=7670642;			
RA	Geissdoerfer W., Ratajczak A., Hillen W.;			
RT	Nucleotide sequence of a putative periplasmic Mn superoxide			
RT	disulphatase from Acinetobacter calcoaceticus ADP1.;			
RL	Gene 186:305-308(1997).			
CC	- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).			
CC	- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Membrane-associated (potential).			
CC	- SIMILARITY: TO THE N-TERMINAL OF BACTERIAL CLASS 1A PENICILLIN-BINDING PROTEINS.			
CC	-----			
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CC	-----			
DR	EMBL: Z46863; CAA86932.1; -			
DR	InterPro: IPR001264; GT_51.			
DR	Pfam: PF00912; Transglycosyl; 1.			
DR	Prodom: PD001895; GT_51; 1.			
KW	peptidoglycan synthesis; Cell wall; Transferase; Transmembrane.			
FT	TRANSMEM 8 30 POTENTIAL.			
SQ	SEQUENCE 224 AA: 26712 MW: 155F114FC14E2FE CRC64;			
Query Match	94.1%;	Score 32;	DB 1;	Length 224;
Best Local Similarity	83.3%;	Pred. No. 26;		
Matches 5;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

OY 1 IQIWI 6
1:||||
DB 19 IQIWI 24

RESULT 2

RR3_ARATH STANDARD: PRT: 218 AA.
ID P56798;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
[1]

SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;
RX MEDLINE=20039611; PubMed=10574454;
RA Sato S., Nakamura Y., Kaneo T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
thaliana";
RL DNA Res. 6:283-290(1999).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.

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CC EMBL: AP000423; BAA84423.1; -;
DR InterPro: IPR004044; KH_TYPE_2;
DR InterPro: IPR001351; Ribosomal_S3.
DR Pfam: PF00189; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR TIGRFAMs: TIGR01009; rpsC_bact; 1.
DR PROSITE: PS50823; KH_TYPE_2; 1.
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
DR Ribosomal protein; Chloroplast.
DOMAIN 47 118 KH TYPE-2.
SEQUENCE 218 AA; 25188 MW; 763CB03FA6D74888 CRC64;

Query Match 88.2%; Score 30; DB 1; Length 218;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWI 6
1:||||
DB 209 IQIWI 214

RR3_SPIOL STANDARD: PRT: 218 AA.
ID P09595;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=89313684; PubMed=2747623;
RA Zhou D.X., Quigley F., Massenet O., Maché R.;
RT "Clonascritpion of the S10- and spc-like operons in spinach
chloroplasts and identification of three of their gene products";
RL Mol. Gen. Genet. 216:439-445(1989).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Geant d'hiver, and cv. Monatol;
RX MEDLINE=21187424; PubMed=11292076;
RA Schmitt-Lineweber C., Maier R.M., Alcatraz J.-P., Cottet A.,
Herrmann R.G., Maché R.;
RT "The plastid chromosome of spinach (Spinacia oleracea): complete
nucleotide sequence and gene organization";
RL Plant Mol. Biol. 45:307-315(2001).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.

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CC EMBL: X13336; CAA31715.1; -;
DR EMBL: AJ400848; CAB88766.1; -;
DR PIR: S01978; R3SP3;
DR InterPro: IPR004044; KH_TYPE_2;
DR InterPro: IPR001351; Ribosomal_S3.
DR Pfam: PF00189; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR TIGRFAMs: TIGR01009; rpsC_bact; 1.
DR PROSITE: PS50823; KH_TYPE_2; 1.
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
DR Ribosomal protein; Chloroplast.
DOMAIN 47 118 KH TYPE-2.
SEQUENCE 218 AA; 24928 MW; 2D2FA40C67431000 CRC64;

Query Match 88.2%; Score 30; DB 1; Length 218;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWI 6
1:||||
DB 209 IQIWI 214

RR3_TOBAC STANDARD: PRT: 218 AA.
ID P06357;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Nicotiana tabacum (Common tobacco).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bright Yellow 4;
RA Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=89313684; PubMed=2747623;
RA Zhou D.X., Quigley F., Massenet O., Maché R.;
RT "Clonascritpion of the S10- and spc-like operons in spinach
chloroplasts and identification of three of their gene products";
RL Mol. Gen. Genet. 216:439-445(1989).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Geant d'hiver, and cv. Monatol;
RX MEDLINE=21187424; PubMed=11292076;
RA Schmitt-Lineweber C., Maier R.M., Alcatraz J.-P., Cottet A.,
Herrmann R.G., Maché R.;
RT "The plastid chromosome of spinach (Spinacia oleracea): complete
nucleotide sequence and gene organization";
RL Plant Mol. Biol. 45:307-315(2001).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.

RA Matsubayashi T., Zaita N., Chunongse J., Obokata J.,
 RA Yamaguchi-Shinozaki K., Ohio C., Torazawa K., Meng B.-Y., Sugita M.,
 RA Dena H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
 RA Tohdo N., Shinada H., Sugita M.,
 RT "The complete nucleotide sequence of the tobacco chloroplast genome:
 RT its gene organization and expression.",
 RL EMOB J. 5:2043-2049(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86287388; PubMed=3016736;
 RA Tanaka M., Wakasugi T., Sugita M., Shinozaki K., Sugita M.,
 RT "Genes for the eight ribosomal proteins are clustered on the
 RT chloroplast genome of tobacco (Nicotiana tabacum): similarity to the
 RT S10 and spc operons of Escherichia coli.",
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6030-6034(1986).
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
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 CC -----
 CC EMBL: 200044; CAA77381.1; -
 DR PIR: A02702; R3NT3.
 DR InterPro: IPR004044; KH_TYPE-2.
 DR InterPro: IPR001351; Ribosomal_S3.
 DR Pfam: PF00189; Ribosomal_S3_C; 1.
 DR Pfam: PF00417; Ribosomal_S3_N; 1.
 DR TIGRFAMS: TIGR01009; rpsc_bact; 1.
 DR PROSITE: PS50823; KH_TYPE-2; 1.
 DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
 KW Ribosomal protein; Chloroplast.
 FT DOMAIN 47 118 KH TYPE-2.
 SQ SEQUENCE 218 AA; 25085 MW; 175D557D37B0D300 CRC64;

Query Match 88.2%; Score 30; DB 1; Length 218;
 Best Local Similarity 83.3%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
 I:||||
 Db 209 IKIWF 214

DLT 5
 ID R3_EPIVI
 AC P30055; STANDARD; PRT; 220 AA.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chloroplast 30S ribosomal protein S3.
 GN RPS3.
 OS Epifagus virginiana (Beechdrops).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eunasterids I; Lamiales; Orchnanchaceae; Epifagus.
 OX NCBI_TaxID=41177;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93066301; PubMed=1332054;
 RA Wolfe K.H., Morden C.W., Palmer J.D.;
 RT "Function and evolution of a minimal plastid genome from a
 RT nonphotosynthetic parasitic plant.",
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93021155; PubMed=1404416;

RA Wolfe K.H., Morden C.W., Ems S.C., Palmer J.D.;
 RT "Rapid evolution of the plastid translational apparatus in a
 RT nonphotosynthetic plant: loss or accelerated sequence evolution of
 RT tRNA and ribosomal protein genes.",
 RL J. Mol. Evol. 35:304-317(1992).
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
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 CC -----
 CC EMBL: M81884; AAA65864.1; -
 DR InterPro: IPR001351; Ribosomal_S3.
 DR Pfam: PF00189; Ribosomal_S3_C; 1.
 DR Pfam: PF00417; Ribosomal_S3_N; 1.
 DR TIGRFAMS: TIGR01009; rpsc_bact; 1.
 DR PROSITE: PS50823; KH_TYPE-2; FALSE_NEG.
 DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
 KW Ribosomal protein; Chloroplast.
 FT DOMAIN 39 120 KH TYPE-2.
 SQ SEQUENCE 220 AA; 25939 MW; 5BF70AC74AB7DF94 CRC64;

Query Match 88.2%; Score 30; DB 1; Length 220;
 Best Local Similarity 83.3%; Pred. No. 61;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
 I:||||
 Db 211 IKIWF 216

RESULT 6
 ID RT03_CHOCR
 AC P48938; STANDARD; PRT; 240 AA.
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Mitochondrial ribosomal protein S3.
 GN RPS3.
 OS Chondrus crispus (Carrageen).
 OG Mitochondrion.
 OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartinales;
 OC Chondrus.
 OX NCBI_TaxID=2769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-APICES;
 RX MEDLINE=95341681; PubMed=7616569;
 RA Leblanc C., Boyen C., Richard O., Bonnard G., Grienenberger J.M.,
 RA Kloareg B.;
 RT "Complete sequence of the mitochondrial DNA of the Rhodophyte
 RT Chondrus crispus (Gigartinales). Gene content and genome
 RT organization.",
 RL J. Mol. Biol. 250:484-495(1995).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL: Z47547; CAA87601.1; -
 DR InterPro: IPR001351; Ribosomal_S3.

DR Pfam: PF00189; Ribosomal_S3_C; 1.
 DR Pfam: PF00417; Ribosomal_S3_N; 1.
 DR PROSITE: PS00548; RIBOSOMAL_S3; FALSE_NEG.
 KW Ribosomal protein; Mitochondrion.
 SQ SEQUENCE 240 AA: 28142 MW: C910AA2E6D8C80DE CRC64:

Query Match 88.2%; Score 30; DB 1; Length 240;
 Best Local Similarity 50.0%; Pred. No. 66;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 QIWIIF 6
 DB 220 QIWIIF 225

RESULT 7
 YL11_CAEEL STANDARD; PRT; 277 AA.

AC Q11098;
 DT 01-NOV-1997 (Rel. 35, Created)
 15-JUN-2002 (Rel. 41, last sequence update)
 15-JUN-2002 (Rel. 41, last annotation update)
 DE Hypothetical protein C02F12.1 in chromosome X.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Polderinae; Caenorhabditis.
 NCBI_TaxID=6239;

RP SEQUENCE FROM N.A.
 RA STRAIN-Bristol N2;
 RL Miller N.;
 RN Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 [2]

REVISIONS.
 RA Waterston R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: SOME, TO THE TETRASPANIN (TM4SF) FAMILY.

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EMBL: G41545; AAK39137.1; -
 WormPep: C02F12.1; CE25749.
 InterPro: IPR000301; Transmem_4.

DR Pfam: PF00335; transmembrane4; 1.
 DR PROSITE: PS00421; TM4_1; FALSE_NEG.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 29 49 POTENTIAL.
 FT TRANSMEM 54 74 POTENTIAL.
 FT TRANSMEM 239 259 POTENTIAL.
 SQ SEQUENCE 277 AA: 31753 MW: 8084221CDBD4C541D CRC64:

Query Match 88.2%; Score 30; DB 1; Length 277;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QIWIIF 6
 DB 238 QIWIIF 242

RESULT 8
 T2G1_HAEGA STANDARD; PRT; 488 AA.
 AC P43418;
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Type II restriction enzyme HgaI (EC 3.1.21.4) (Endonuclease HgaI)
 DE (R.HgaI).
 GN HGAIR.
 OS Haemophilus gallinarum.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 NCBI_TaxID=728;

RP SEQUENCE FROM N.A.
 RA STRAIN-NCTC 3438;
 RC Sugisaki H.;
 RT "Nucleotide sequence of the gene of HgaI restriction endonuclease";
 RL Bull. Inst. Chem. Res., Kyoto Univ. 71:338-342(1993).

CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCES GACGC AND GCCTC
 CC AND CLEAVES RESPECTIVELY 10 BASES AFTER G-1 AND 10 BASES BEFORE
 CC G'-1.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.

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EMBL: D17388; BAA04208.1; -
 DR REBASE: 1096; HgaI.
 KW Hydrolyase; Endonuclease; Nuclease; Restriction system.
 SQ SEQUENCE 488 AA: 56737 MW: B5E05259E3C710D2 CRC64:

Query Match 88.2%; Score 30; DB 1; Length 488;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QIWIIF 6
 DB 11 QIWIIF 15

RESULT 9
 Y052_BUCAI STANDARD; PRT; 144 AA.
 AC P57160;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Hypothetical protein BU052.

GN BU052.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.

NCBI_TaxID=118099;

RP SEQUENCE FROM N.A.

RA MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;

RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS";
 RL Nature 407:81-86(2000).

CC -1- SIMILARITY: STRONG, TO E. COLI Y1BN AND H. INFLUENZAE HI0744.

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CC -----
DR EMBL: AP001118; BAB12775.1; -
DR InterPro: IPR001763; Rhodanese-like.
DR Pfam: PF00581; Rhodanese; 1.
DR SMART: SM00450; RHOD; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 144 AA; 16921 MW; 87D669CDAD999ECB CRC64;

Query Match 85.3%; Score 29; DB 1; Length 144;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 IQIWIIF 6
1 : : : : :
DB 15 ISIWIIF 20

RESULT 10
RR3_MESVI STANDARD; PRT; 213 AA.
O9MU02;
DR 16-OCT-2001 (Rel. 40, Created)
DR 16-OCT-2001 (Rel. 40, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIES-296;
RX MEDLINE-20150907; PubMed-1068199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancstral chloroplast genome in Mesostigma viride reveals an early
branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
CC
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CC -----

DR EMBL: AF16114; AAF3809.1; -
DR InterPro: IPR004044; KH_TYPE_2.
DR InterPro: IPR004087; KH_dom.
DR InterPro: IPR001351; Ribosomal_S3.
DR Pfam: PF00013; KH-domain; 1.
DR Pfam: PF00189; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR SMART: SM00322; KH; 1.
DR TIGRfams: TIGR01009; rpsC_bact; 1.
DR PROSITE: PS50823; KH_TYPE_2; 1.
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; Chloroplast.
FT DOMAIN 39 109 KH TYPE-2.
SQ SEQUENCE 213 AA; 24545 MW; 1C7ECC9A7B8A7CD CRC64;

Query Match 85.3%; Score 29; DB 1; Length 213;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWIIF 6
1 : : : : :
DB 200 IKWIIF 205

RESULT 11
RR3_MARPO STANDARD; PRT; 217 AA.
AC P06356;
DR 01-JAN-1988 (Rel. 06, Created)
DR 01-JAN-1988 (Rel. 06, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Marchantia polymorpha (liverwort).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiales;
OC Marchantiaceae; Marchantia.
OX NCBI_TaxID=3197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89068687; PubMed-3199436;
RA Fukuzawa H., Kohchi T., Sano T., Shirai H., Umesono K., Inokuchi H.,
RA Ozeki H., Ohyama K.,
RT "Structure and organization of Marchantia polymorpha chloroplast
genome. III. Gene organization of the large single copy region from
rbcL to trnI(CAU).";
RL J. Mol. Biol. 203:333-351(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
RA Ozeki H.;

RT "Chloroplast gene organization deduced from complete sequence of
liverwort Marchantia polymorpha chloroplast DNA.";
RL Nature 322:572-574(1986).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
CC
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CC -----

DR EMBL: X04465; CAA28124.1; -
DR PIR: A02701; R3LV3.
DR InterPro: IPR004044; KH_TYPE_2.
DR InterPro: IPR001351; Ribosomal_S3.
DR Pfam: PF00189; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR TIGRfams: TIGR01009; rpsC_bact; 1.
DR PROSITE: PS50823; KH_TYPE_2; 1.
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; Chloroplast.
FT DOMAIN 46 117 KH TYPE-2.
SQ SEQUENCE 217 AA; 25055 MW; 7AF3CA7834B8A01 CRC64;

Query Match 85.3%; Score 29; DB 1; Length 217;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWIIF 6
1 : : : : :
DB 208 IKWIIF 213

RESULT 12
RR3_MAIZE STANDARD; PRT; 224 AA.
AC P06586;
DR 01-JAN-1988 (Rel. 06, Created)
DR 01-JAN-1988 (Rel. 06, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Zea mays (Maize).
OC Chloroplast.
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC clade;
OC Panicoideae: Andropogoneae: Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87231045; PubMed=3588305;
RA McLaughlin W.E., Larrina I.M.;
RT "The sequence of the maize plastid encoded rps3 locus.";
RL Nucleic Acids Res. 15:4689-4689(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95395841; PubMed=7666415;
RA Mäler R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
hotspots of divergence and fine tuning of genetic information by
transcript editing.";
RL J. Mol. Biol. 251:614-628(1995).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y00340; CAA68427.1; -
DR EMBL: X86563; CAA60324.1; -
DR MaizeDB: 66303; -
DR InterPro: IPR001351; Ribosomal_S3.
DR Pfam: PF00417; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR TIGRFAMs: TIGR01009; rpsC_bact; 1.
DR PROSITE: PS50823; KH_TYPE_2; FALSE_NEG.
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; Chloroplast.
FT DOMAIN 43 124 KH TYPE-2.
SQ SEQUENCE 224 AA; 25916 MW; B6B8B6BA8AF70DA CRC64;

Query Match
Best Local Similarity 85.3%; Score 29; DB 1; Length 224;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 IQIWF 6
:|||||
215 VKIWF 220

RESULT 13
RR3_CHLVU STANDARD: PRT; 231 AA.
AC P56365;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Chlorella vulgaris.
OC Chloroplast.
OC Eukaryota: Viridiplantae: Chlorophyta: Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=IAM C-27 / Tam1ya;
RX MEDLINE=97303241; PubMed=9159184;

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RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
RA Inamura A., Yoshinaga K., Sugita M.;
RT "Complete nucleotide sequence of the chloroplast genome from the
RT green alga Chlorella vulgaris: the existence of genes possibly
RT involved in chloroplast division.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB001684; BAA58006.1; -
DR InterPro: IPR004044; KH_TYPE_2.
DR InterPro: IPR001351; Ribosomal_S3.
DR Pfam: PF00189; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR TIGRFAMs: TIGR01009; rpsC_bact; 1.
DR PROSITE: PS50823; KH_TYPE_2; 1.
DR PROSITE: PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; Chloroplast.
FT DOMAIN 39 123 KH TYPE-2.
SQ SEQUENCE 231 AA; 26404 MW; D3EDE90A93551097 CRC64;

Query Match
Best Local Similarity 85.3%; Score 29; DB 1; Length 231;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 IQIWF 6
:|||||
214 IKIWF 219

RESULT 14
RR3_ORYSA STANDARD: PRT; 239 AA.
AC P12146;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Oryza sativa (Rice).
OC Chloroplast.
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RX MEDLINE=89364698; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugita M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct tRNA genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RL Mol. Gen. Genet. 217:185-194(1989).
CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
CC -----
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EMBL: X15901; CAA33934.1; -

DR PIR: J00265; R3R23

DR InterPro: IPR001351; Ribosomal_S3.

DR Pfam: PF00189; Ribosomal_S3_C; 1.

DR Pfam: PF00417; Ribosomal_S3_N; 1.

DR TIGRFAMs: TIGR01009; rpsc_bact; 1.

DR PROSITE: PS50823; KH_type_2; FALSE-NEG.

DR PROSITE: PS00548; RIBOSOMAL_S3; 1.

KW Ribosomal protein; Chloroplast.

FT DOMAIN 43 139 KH_type-2.

SQ SEQUENCE 239 AA; 27518 MW; 3152AC028BFCC139 CRC64;

Query Match

Best Local Similarity 85.3%; Score 29; DB 1; Length 239;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 IQIWIIF 6

Db 230 VKIWIIF 235

RESULT 15

RS3_SYNY3 STANDARD; PRT; 239 AA.

AC P73314:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 30S ribosomal protein S3.

GN RPS3 OR RPS3 OR SLI1804.

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_TaxId=1148;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97061201; PubMed=8905231;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;

RA "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";

RT DNA Res. 3:109-136(1996).

RT -i- FUNCTION: THIS PROTEIN IS INVOLVED IN THE BINDING OF INITIATOR MET-TRNA (BY SIMILARITY).

CC -i- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.

CC -i- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.

CC -----

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CC -----

CC EMBL: D90905; BAA17343.1; -

DR InterPro: IPR004044; KH_type_2.

DR InterPro: IPR004087; KH_dom.

DR InterPro: IPR004086; KH_type_1.

DR InterPro: IPR001351; Ribosomal_S3.

DR Pfam: PF00013; KH-domain; 1.

DR Pfam: PF00189; Ribosomal_S3_C; 1.

DR Pfam: PF00417; Ribosomal_S3_N; 1.

DR SMART: SM00322; KH; 1.

DR TIGRFAMs: TIGR01009; rpsc_bact; 1.

DR PROSITE: PS50823; KH_type_2; 1.

DR PROSITE: PS00548; RIBOSOMAL_S3; 1.

KW Ribosomal protein; trna-binding; Complete proteome.

FT INIT_MET 0

FT DOMAIN 64 100 KH_type-2.

SQ SEQUENCE 239 AA; 27016 MW; 066ACE072B38CB2 CRC64;

Query Match

Best Local Similarity 85.3%; Score 29; DB 1; Length 239;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 IQIWIIF 6

Db 199 IKWIIF 204

Search completed: January 3, 2003, 15:29:22

Job time : 6.18182 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:24:35 ; Search time 20.3182 Seconds
(without alignments)
60.846 Million cell updates/sec

Title: US-09-543-188a-21

Perfect score: 34
Sequence: 1 IOIWF 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriap:*
- 17: sp-archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	97.1	282	8 09Z2N7	09Z2N7 cyanidiosch
2	33	97.1	285	5 017997	017997 caenorhabd
3	33	97.1	360	16 09KCM4	09KCM4 bacillus ha
4	32	94.1	86	10 09MOC7	09MOC7 arabidopsis
5	32	94.1	88	10 09ZV45	09ZV45 arabidopsis
6	32	94.1	291	16 09CLF4	09CLF4 pasteurella
7	32	94.1	495	8 063853	063853 sarcophyton
8	31	91.2	320	2 093HD9	093HD9 streptomyce
9	31	91.2	394	16 09PMP4	09PMP4 campylobact
10	31	91.2	719	2 08RPJ4	08RPJ4 desulfatoba
11	30	88.2	115	11 09CU03	09CU03 mus musculu
12	30	88.2	218	8 09MT17	09MT17 oenothera h
13	30	88.2	218	10 08S8V5	08S8V5 atropa bell
14	30	88.2	229	16 066753	066753 aquilex aeo
15	30	88.2	246	3 09P3R7	09P3R7 neurospora
16	30	88.2	320	2 09RNE1	09RNE1 bacillus an

17	30	88.2	344	17 0973N4	0973N4 sulfolobus
18	30	88.2	364	2 085468	085468 bacillus ce
19	30	88.2	403	17 09HLS6	09HLS6 thermoplas
20	30	88.2	427	17 097C83	097C83 thermoplas
21	30	88.2	563	10 08WOK1	08WOK1 oryza sativ
22	29	85.3	107	5 061555	061555 drosophila
23	29	85.3	164	11 08R460	08R460 mus musculu
24	29	85.3	218	8 098455	098455 spirogyra m
25	29	85.3	218	8 09BBP8	09BBP8 lotus japon
26	29	85.3	219	16 08RIG1	08RIG1 fusobacteri
27	29	85.3	221	8 09T120	09T120 nephruselm
28	29	85.3	222	16 097P66	097P66 streptococc
29	29	85.3	235	16 09CL37	09CL37 pasteurella
30	29	85.3	239	8 095H49	095H49 triticum ae
31	29	85.3	243	16 08UE24	08UE24 agrobacteri
32	29	85.3	244	8 099992	099992 porphyra pu
33	29	85.3	252	2 08VOR8	08VOR8 physocystis
34	29	85.3	255	11 09C2V2	09C2V2 mus musculu
35	29	85.3	327	16 P74743	P74743 synchocyst
36	29	85.3	348	16 051706	051706 borrelia bu
37	29	85.3	373	5 061643	061643 drosophila
38	29	85.3	417	3 09C473	09C473 emericella
39	29	85.3	523	8 09G8Q4	09G8Q4 naegleria g
40	29	85.3	553	10 064861	064861 arabidopsis
41	29	85.3	616	17 09HIF5	09HIF5 thermoplas
42	29	85.3	678	5 08MR60	08MR60 drosophila
43	29	85.3	720	10 09SPF9	09SPF9 arabidopsis
44	29	85.3	720	10 09SPF8	09SPF8 arabidopsis
45	29	85.3	720	10 080809	080809 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q9Z2N7	PRELIMINARY;	PRT;	282 AA.
AC	Q9Z2N7			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	30S ribosomal protein S3.			
GN	RPS3.			
OS	Cyanidioschyzon merolae.			
OG	Mitochondrion.			
OC	Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.			
OX	NCBI_TaxID=45157;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=10D;			
RX	MEDLINE=99030526; PubMed=9801318;			
RA	Ohta N., Sato N., Kuroiwa T.;			
RT	"Structure and organization of the mitochondrial genome of the			
RT	unicellular red alga Cyanidioschyzon merolae deduced from the complete			
RT	nucleotide sequence."			
RL	Nucleic Acids Res. 26:5190-5198(1998).			
DR	EMBL; D89861; BAA36537.1.-.			
DR	InterPro; IPR001351; Ribosomal_S3.			
DR	Pfam; PF00189; Ribosomal_S3_C; 1.			
KW	Mitochondrion; Ribosomal protein.			
SO	SEQUENCE 282 AA; 33871 MW; 89CC910DAA22DFB2 CRC64;			

Query Match 97.1%; Score 33; DB 8; Length 282;
Best local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IOIWF 6
Db 275 IOIWF 280

RESULT 2
017997

ID 017997 PRELIMINARY: PRT: 285 AA.
AC 017997;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE R10012.11 protein.
GN R10012.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RL Percy C.M.;
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
Science 282:2012-2018(1998).
DR EMBL: Z81109; CAB03254.1; -
DR InterPro: IPR003003; 7TM_chemo2.
DR InterPro: IPR00168; 7TM_nematode.
DR Pfam: PF01604; 7tm_5; 1.
SQ SEQUENCE 285 AA; 32927 MW; C3078F66F3561CBD CRC64;

Query Match 97.1%; Score 33; DB 5; Length 285;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWF 6
DB 48 VOIWF 53

RESULT 3

ID 09KCM4 PRELIMINARY: PRT: 360 AA.
AC 09KCM4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Spore germination protein.
GN BH1455
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kohara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis";
Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001512; BAB05174.1; -
KN Complete proteome.
SQ SEQUENCE 360 AA; 41587 MW; 1B25DCA9DAF6E328 CRC64;

Query Match 97.1%; Score 33; DB 16; Length 360;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWF 6
DB 109 IOIWF 114

RESULT 4

ID 09MOC7 PRELIMINARY: PRT: 86 AA.
AC 09MOC7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Small nuclear ribonucleoprotein homolog.
GN ATG630330.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL161576; CAB81026.1; -
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
KW Nucleocapsid; Ribonucleoprotein.
SQ SEQUENCE 86 AA; 10097 MW; E5AD9FDF35C3AC0D CRC64;

Query Match 94.1%; Score 32; DB 10; Length 86;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWF 6
DB 27 IOIWF 32

RESULT 5

ID 09ZV45 PRELIMINARY: PRT: 88 AA.
AC 09ZV45;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative small nuclear ribonucleoprotein E.
GN AT2G18740.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Motilal K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nietman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AC005724; AAD08943.1; -
DR InterPro: IPR001163; snRNP_Sm.

DR Pfam: PF01423; Sm; 1.
 KM Nucleocapsid; Ribonucleoprotein.
 SQ SEQUENCE 88 AA; 10298 MW; 762719DD9DFD35C5 CRC64;

Query Match
 Best Local Similarity 94.1%; Score 32; DB 10; Length 88;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
 |||||:
 DB 27 IOIWL 32

RESULT 6
 O9CLF4 PRELIMINARY; PRT; 291 AA.

ID O9CLF4
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 RT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 GN Hypothetical protein PM1281.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida PM70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL: AF006167; AAK03365.1; -;
 DR InterPro: IPR004626; RARD; 1.
 DR TIGFAMS: TIGR00688; rard; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 291 AA; 32530 MW; 43F47FDE6986512B CRC64;

Query Match
 Best Local Similarity 94.1%; Score 32; DB 16; Length 291;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
 |||||:
 DB 84 IOIWL 89

RESULT 7
 O63853 PRELIMINARY; PRT; 495 AA.

ID O63853
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 RT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 GN NADH dehydrogenase subunit 4.
 OS ND4.
 OS Sarcophyton glaucum.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Alcyonacea;
 OC Alcyonidae; Sarcophyton.
 OX NCBI_TaxID=70919;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99065763; PubMed=9847412;
 RA Beaton M.J., Roger A.J., Cavalier-Smith T.;
 RT "Sequence analysis of the mitochondrial genome of Sarcophyton glaucum:
 RT conserved gene order among octocorals.";
 RL J. Mol. Evol. 47:697-708(1998).
 DE [2]
 GN SEQUENCE OF 450-495 FROM N.A.
 RP MEDLINE=98210232; PubMed=9541536;
 RX Pont-Kington G., Okada N.A., Macfarlane J.L., Beagley C.T.,

RA Watkins-Sims C.D., Cavalier-Smith T., Clark-Walker G.D.,
 RA Wolstenholme D.R.;
 RT "Mitochondrial DNA of the coral Sarcophyton glaucum contains a gene
 RT for a homologue of bacterial Puts: a possible case of gene transfer
 RT from the nucleus to the mitochondrion.";
 RL J. Mol. Evol. 46:419-431(1998).
 CC -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 DR EMBL: AF064823; AAC99651.1; -;
 DR EMBL: AF063192; AAC16387.1; -;
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; oxidored_q1; 1.
 DR PRINTS: PR01559; DUFFYANTIGEN.
 KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 SQ SEQUENCE 495 AA; 55419 MW; 6E0C04C478A5C8B4 CRC64;

Query Match
 Best Local Similarity 94.1%; Score 32; DB 8; Length 495;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
 |||||:
 DB 219 IOIWL 224

RESULT 8
 O93HD9 PRELIMINARY; PRT; 320 AA.

ID O93HD9
 AC O93HD9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 RT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 GN ABC transporter.
 OS Streptomyces avermitilis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinohe M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: Deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 DR EMBL: AB070945; BAB69249.1; -;
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp; 1.
 DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN 1.
 SQ SEQUENCE 320 AA; 34176 MW; DD3BC5AB26756426 CRC64;

Query Match
 Best Local Similarity 91.2%; Score 31; DB 2; Length 320;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
 :|||:
 DB 308 YOLWIF 313

RESULT 9
 O9PMP4 PRELIMINARY; PRT; 394 AA.

ID O9PMP4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 RT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 GN Possible polysaccharide modification protein.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.

```

OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parthill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagsals K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL: AL139078; CAB73837.1; -.
KM Complete proteome.
SQ SEQUENCE 394 AA; 46938 MW; E4293DB5879FD64E CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 16; Length 394;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 IRTWIF 110

RESULT 10
OBRP4 PRELIMINARY; PRT; 719 AA.
AC OBRP4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
OS Hypothetical 80.1 kDa protein.
OC Desulfitobacterium hafnense.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Peptococcaceae; Desulfitobacterium.
OX NCBI_TaxID=49338;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DCB-2;
RA Davis J.K., Tiedje J.M.;
RT "Sequence and transcriptional analysis of reductive dehalogenase genes
RT of Desulfitobacterium."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF403182; AAL87758.1; -.
KM Hypothetical protein.
SQ SEQUENCE 719 AA; 80119 MW; B806F0F0FID79B CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 2; Length 719;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOWIF 6
Db 108 IOWIF 113

RESULT 11
O9CU03 PRELIMINARY; PRT; 115 AA.
AC O9CU03;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1700116B05R1k protein (fragment).
GN 1700116B05R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schmil L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta Y., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuk S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK018963; BAB31497.1; -.
DR MGD: MGI:1925889; 1700116B05R1k.
FT NON_TER 1
SQ SEQUENCE 115 AA; 12580 MW; F95076419A6A6B9C CRC64;

Query Match
Best Local Similarity 88.2%; Score 30; DB 11; Length 115;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOWIF 6
Db 40 IRTWIF 45

RESULT 12
O9MT17 PRELIMINARY; PRT; 218 AA.
AC O9MT17;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Ribosomal protein S3.
GN RPS3.
OS Oenothera hookeri (Hooker's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=85636;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20309318; PubMed=10852478;
RA Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Mater R.M.,
RA Chiu W.L., Sears B.;
RT "Complete nucleotide sequence of the Oenothera elata plastid
RT chromosome, representing plastome I of the five distinguishable
RT Oenothera plastomes."
RL Mol. Gen. Genet. 263:581-585(2000).
DR EMBL: AJ271079; CAB67198.1; -.
DR InterPro: IPR004044; KH_TYPE_2.
DR Pfam: PF00189; Ribosomal_S3_C; 1.
DR Pfam: PF00417; Ribosomal_S3_N; 1.
DR TIGRFAMs: TIGR01009; rpsC_bact; 1.
DR PROSITE: PS50823; KH_TYPE_2; 1.
DR PROSITE: PS00548; RIBOSOMAL_S3; UNKNOWN_1.
KM Chloroplast.
SQ SEQUENCE 218 AA; 24971 MW; B0B741F658B010BA CRC64;

Query Match
Best Local Similarity 88.2%; Score 30; DB 8; Length 218;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
 QY 1 IQIWF 6
 1:||||
 Db 210 IKIWF 215

RESULT 13

OS8SV5 PRELIMINARY: PRT: 218 AA.

ID OS8SV5

AC OS8SV5:

DT 01-JUN-2002 (TRENBLREL. 21, Created)

DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)

DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)

DE Ribosomal protein S3.

GN RPS3.

OS Atropa belladonna (belladonna) (deadly nightshade).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Atropa.

NCBI_TaxID=33113;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AB5P(KAN);

RA Schmitz-Linneweber C., Regel R., Gia Du T., Hupfer H., Herrmann R.G.,

Maler R.M.;

RT "The nucleotide sequence of the plastid chromosome of *Atropa*

belladonna (deadly nightshade) and its comparison with that of

Nicotiana tabacum with emphasis on sequence elements relevant for

microevolution."

RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ316582; CAC88082.1; -

SQ SEQUENCE 218 AA; 25042 MW; 115967F1CCED2F9 CRC64;

Query Match 88.2%; Score 30; DB 10; Length 218;

Best Local Similarity 83.3%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
 1:||||
 Db 209 IKIWF 214

RESULT 14

ID 066753

AC 066753: PRELIMINARY: PRT: 229 AA.

DT 01-AUG-1998 (TRENBLREL. 07, Created)

DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)

DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)

DE Glutaredoxin-like protein.

GN GUA OR AQ.443.

OS Aquifex aeolicus.

OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

NCBI_TaxID=63363;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VF5;

RA MEDLINE=98196666; PubMed=9537320;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay N., Huber R.,

Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;

RT "The complete genome of the hyperthermophilic bacterium *Aquifex*

aeolicus."

RL Nature 392:353-358(1998).

DR EMBL: AE000690; AAC06709.1; -

DR InterPro: IPR000063; ThioRed.

DR InterPro: IPR000531; TonB_boxC.

DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 229 AA; 25640 MW; C3A3C141FE05B25E CRC64;

Query Match 88.2%; Score 30; DB 16; Length 229;

Best Local Similarity 66.7%; Pred. No. 3.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
 1:||||
 Db 138 IETWLF 143

RESULT 15

09P3R7 PRELIMINARY: PRT: 246 AA.

ID 09P3R7

AC 09P3R7:

DT 01-OCT-2000 (TRENBLREL. 15, Created)

DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)

DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)

DE Related to cell protein.

GN B24P7.180.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;

RM [1]

RP SEQUENCE FROM N.A.

RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,

Myakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.

RP [2]

RA German Neurospora genome project;

Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL: AL389890; CAB97283.2; -

DR InterPro: IPR005103; Glyco_hydro_61.

DR Pfam: PF03443; Glyco_hydro_61; 2.

SQ SEQUENCE 246 AA; 26817 MW; 30E4F3436791A92A CRC64;

Query Match 88.2%; Score 30; DB 3; Length 246;

Best Local Similarity 50.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
 1:||||
 Db 98 YQVWLF 103

Search completed: January 3, 2003, 15:32:02
 Job time : 23.3182 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:16 : Search time 9 Seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-543-188A-21

Perfect score: 34

Sequence: 1 IQIWMF 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Indexed: 262574 seqs, 29422922 residues

Minimal number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	88.2	70	4	US-09-288-143-114
2	29	85.3	391	3	US-08-968-563-11
3	29	85.3	391	4	US-08-969-683A-11
4	29	85.3	391	4	US-09-297-928-7
5	29	85.3	433	2	US-08-919-624-1
6	28	82.4	68	4	US-09-025-151-18
7	28	82.4	287	3	US-09-065-474-145
8	28	82.4	287	4	US-09-557-034-145
9	28	82.4	312	2	US-09-031-485-2
10	28	82.4	312	2	US-08-847-429A-2
11	28	82.4	312	3	US-09-065-474-2
12	28	82.4	312	4	US-09-557-034-2
13	28	82.4	413	4	US-09-134-001C-5503
14	28	82.4	496	4	US-09-134-001C-3703
15	28	82.4	591	4	US-09-134-001C-3705
16	28	82.4	1745	2	US-09-031-485-33
17	28	82.4	1745	2	US-08-847-429A-33
18	28	82.4	1745	3	US-09-065-474-33
19	28	82.4	1745	4	US-09-557-034-33
20	27	79.4	15	1	US-08-148-160-2
21	27	79.4	51	1	US-07-791-213D-1
22	27	79.4	51	1	US-07-791-213D-2
23	27	79.4	51	1	US-07-791-213D-7
24	27	79.4	51	1	US-07-791-213D-17
25	27	79.4	51	1	US-07-972-387-67
26	27	79.4	51	1	US-08-431-412-67
27	27	79.4	51	1	US-08-057-971-67

28	27	79.4	51	1	US-08-293-150A-1	Sequence 1, Appl
29	27	79.4	51	1	US-08-293-150A-2	Sequence 2, Appl
30	27	79.4	51	1	US-08-293-150A-7	Sequence 7, Appl
31	27	79.4	51	1	US-08-293-150A-17	Sequence 17, Appl
32	27	79.4	54	1	US-07-791-213D-16	Sequence 16, Appl
33	27	79.4	54	1	US-08-293-150A-16	Sequence 16, Appl
34	27	79.4	58	1	US-07-700-526-11	Sequence 11, Appl
35	27	79.4	58	1	US-08-384-489-11	Sequence 11, Appl
36	27	79.4	58	1	US-08-358-160-3	Sequence 3, Appl
37	27	79.4	58	1	US-08-358-160-75	Sequence 75, Appl
38	27	79.4	58	1	US-08-463-155A-39	Sequence 39, Appl
39	27	79.4	58	1	US-08-463-432B-47	Sequence 47, Appl
40	27	79.4	58	1	US-08-676-125A-47	Sequence 47, Appl
41	27	79.4	58	1	US-08-206-310A-39	Sequence 39, Appl
42	27	79.4	58	1	US-08-398-010A-39	Sequence 39, Appl
43	27	79.4	58	2	US-08-398-628A-39	Sequence 39, Appl
44	27	79.4	58	2	US-08-399-115A-39	Sequence 39, Appl
45	27	79.4	58	2	US-09-136-012A-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-09-288-143-114
; Sequence 114, Application US/09288143
; Patent No. 6433139
; GENERAL INFORMATION:
; APPLICANT: Brewer et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P1
; CURRENT APPLICATION NUMBER: US/09/288,143
; EARLIER APPLICATION NUMBER: PCT/US98/21142
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,463
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,529
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/071,498
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,527
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,536
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,532
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals stop translation
US-09-288-143-114
Query Match 88.2% Score 30; DB 4; Length 70;
Best Local Similarity 50.0% Pred. No. 1.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0;
Gaps 0;
Oy 1 IQIWMF 6
Db 15 LQWVWF 20
RESULT 2
US-08-968-563-11
; Sequence 11, Application US/08968563
; Patent No. 6013494
; GENERAL INFORMATION:

APPLICANT: CHARLES E. NAKAMURA
APPLICANT: ANTHONY A. GATENBY
APPLICANT: AMY (KUANG-HUA) HSU
APPLICANT: RICHARD D. LA REAU
APPLICANT: SHARON L. HAYNIE
APPLICANT: MARIA DIAZ-FORRES
APPLICANT: DONALD E. TRIMBER
APPLICANT: GREGORY M. WHITED
APPLICANT: VASANTHA NAGARAJAN
APPLICANT: MARK S. PAYNE
APPLICANT: STEPHEN K. PICATAGGIO
APPLICANT: RAMESH V. NAIR
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,601
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMENHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9982
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: GPD1
US-08-968-563-11

Query Match 85.3%; Score 29; DB 3; Length 391;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWF 6
:|:|:|
Db 68 VQMWVF 73

RESULT 3
US-08-969-683A-11
Sequence 11, Application US/08969683A
Patent No. 6136576
GENERAL INFORMATION:
APPLICANT: GENENCOR INTERNATIONAL, INC.

TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3 PROPANEDIOL
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 4 Cambridge Place
STREET: 1870 South Winton road
CITY: Rochester
STATE: NY
COUNTRY: U.S.A
ZIP: 14618
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,683A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20873
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: 60/030,601
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC 369-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-864-7620
TELEFAX: 650-845-6504
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: GPD1
US-08-969-683A-11

Query Match 85.3%; Score 29; DB 4; Length 391;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQIWF 6
:|:|:|
Db 68 VQMWVF 73

RESULT 4
US-09-297-928-7
Sequence 7, Application US/09297928
Patent No. 6358716
GENERAL INFORMATION:
APPLICANT: BULTHUIS, BEN A.
GATENBY, ANTHONY A.
HAYNIE, SHARON L.
HSU, AMY K.
LAREAU, RICHARD D.
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
GLYCEROL BY RECOMBINANT
ORGANISMS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STATE: NEW YORK

COUNTRY: U.S.A.
ZIP: 14618
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/297,928
FILING DATE: 11-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/03602
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9981-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
TELEX: 6717325
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-297-928-7

Query Match
Best Local Similarity 85.3%; Score 29; DB 4; Length 391;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
||:|:|
Db 68 VQMWVF 73

RESULT 5
US-08-919-624-1
Sequence 1, Application US/08919624
Patent No. 5994097
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,624
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0377 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CARDNOT01
CLONE: 282414
US-08-919-624-1

Query Match
Best Local Similarity 85.3%; Score 29; DB 2; Length 433;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IQIWF 6
||:|:|
Db 162 ISIWIF 167

RESULT 6
US-09-025-151-18
Sequence 18, Application US/09025151
Patent No. 6187535
GENERAL INFORMATION:
APPLICANT: Legrain, Pierre
APPLICANT: Fromont, Micheline
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: FAST AND EXHAUSTIVE METHOD FOR SELECTING A PREY
TITLE OF INVENTION: POLYPEPTIDE INTERACTING WITH A BAIT POLYPEPTIDE OF
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS OF
TITLE OF INVENTION: INTERACTORS POLYPEPTIDES
FILE REFERENCE: 03495-0164
CURRENT APPLICATION NUMBER: US/09/025,151
CURRENT FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 68
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-025-151-18

Query Match
Best Local Similarity 82.4%; Score 28; DB 4; Length 68;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
||:|:|
Db 7 IQVWLY 12

RESULT 7
US-09-065-474-145
Sequence 145, Application US/09065474
Patent No. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins

STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-065-474-145

Query Match
Best Local Similarity 82.4%; Score 28; DB 3; Length 287;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
DB 11 LRIMIF 16

RESULT 8
US-09-557-034-145
Sequence 145, Application US/09557034
Patent No. 6365569
GENERAL INFORMATION:
APPLICANT: Tang, Liang
Blehm, E. Scot
TITLE OF INVENTION: DIOFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,034
FILING DATE: 21-APR-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/065,474
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-09-557-034-145

Query Match
Best Local Similarity 82.4%; Score 28; DB 4; Length 287;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
DB 11 LRIMIF 16

RESULT 9
US-09-031-485-2
Sequence 2, Application US/09031485
Patent No. 5824306
GENERAL INFORMATION:
APPLICANT: Tang, Liang
Blehm, E. Scot
TITLE OF INVENTION: DIOFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-031-485-2

Query Match
Best Local Similarity 82.4%; Score 28; DB 2; Length 312;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
DB 159 LRIMIF 164

RESULT 10
US-08-847-429A-2
Sequence 2, Application US/08847429A
Patent No. 5827692
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429A
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-847-429A-2
Query Match 82.4%; Score 28; DB 2; Length 312;
Best Local Similarity 66.7%; Pred. No. 9.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 IQIWI 6
:|||||
Db 159 LRIWI 164

RESULT 11
US-09-065-474-2
Sequence 2, Application US/09065474
Patent No. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/484-9505
TELEFAX: 970/493-7272
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-065-474-2
Query Match 82.4%; Score 28; DB 3; Length 312;
Best Local Similarity 66.7%; Pred. No. 9.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 IQIWI 6
:|||||
Db 159 LRIWI 164

RESULT 12
US-09-557-034-2
Sequence 2, Application US/09557034
Patent No. 6365569
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,034
FILING DATE: 21-APR-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/065,474
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/484-9505
TELEFAX: 970/493-7272
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-557-034-2

Query Match 82.4%; Score 28; DB 4; Length 312;
Best Local Similarity 66.7%; Pred. NO. 9.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
:|||||
Db 159 LRIWIF 164

RESULT 13
US-09-134-001C-5503
Sequence 5503, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5503
LENGTH: 413
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5503

Query Match 82.4%; Score 28; DB 4; Length 413;
Best Local Similarity 80.0%; Pred. NO. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QIWF 6
:|||||
Db 110 QIWF 114

RESULT 14
US-09-134-001C-3703
Sequence 3703, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3703
LENGTH: 496
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3703

Query Match 82.4%; Score 28; DB 4; Length 496;
Best Local Similarity 50.0%; Pred. NO. 1.5e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 157 MOLWIF 162
:|:|:|

RESULT 15
US-09-134-001C-3275
Sequence 3275, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3275
LENGTH: 591
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3275

Query Match 82.4%; Score 28; DB 4; Length 591;
Best Local Similarity 66.7%; Pred. NO. 1.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IQIWF 6
:|||||
Db 359 VNIWIF 364

Search completed: January 3, 2003, 15:34:30
Job time : 10 secs

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OW protein - protein search, using sw model

Run on: January 3, 2003, 15:32:11 ; Search time 4.77273 Seconds
(without alignments)
23.825 Million cell updates/sec

Title: US-09-543-188a-21

Perfect score: 34
Sequence: 1 IQIWI 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

al number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published.Applications-AA:*
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4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	85.3	179	10	US-09-789-561-92
2	29	85.3	261	10	US-09-789-561-169
3	28	82.4	82	10	US-09-864-761-47624
4	28	82.4	92	9	US-09-736-457-331
5	28	82.4	92	9	US-09-902-941-331
6	28	82.4	92	9	US-09-849-626-331
7	28	82.4	95	10	US-09-925-300-1436
8	28	82.4	228	10	US-09-815-242-5172
9	28	82.4	233	10	US-09-741-669-319
10	28	82.4	233	10	US-09-913-020-386
11	28	82.4	233	10	US-09-815-242-10353
12	28	82.4	233	10	US-09-815-242-13969
13	28	82.4	234	10	US-09-815-242-11592
14	28	82.4	235	10	US-09-815-242-11103
15	28	82.4	293	9	US-09-738-626-3652
16	28	82.4	314	10	US-09-886-055-495
17	27	79.4	39	10	US-09-764-877-1254
18	27	79.4	66	10	US-09-815-242-5869
19	27	79.4	87	9	US-09-796-692-1581

20	27	79.4	110	10	US-09-867-550-298	Sequence 298, App
21	27	79.4	264	10	US-09-925-301-905	Sequence 905, App
22	27	79.4	283	9	US-09-970-989-2	Sequence 2, Appl1
23	27	79.4	366	10	US-09-925-301-1175	Sequence 1175, Ap
24	27	79.4	384	9	US-09-738-626-6166	Sequence 6166, Ap
25	27	79.4	411	10	US-09-901-252-16	Sequence 16, Appl
26	27	79.4	466	10	US-09-804-551B-14	Sequence 14, Appl
27	27	79.4	572	10	US-09-815-242-5626	Sequence 5626, Ap
28	27	79.4	573	10	US-09-815-242-12247	Sequence 12247, A
29	27	79.4	573	10	US-09-815-242-12921	Sequence 12921, A
30	27	79.4	608	10	US-09-924-356-8	Sequence 8, Appl1
31	27	79.4	803	10	US-09-815-242-5597	Sequence 5597, Ap
32	27	79.4	805	10	US-09-815-242-12286	Sequence 12286, A
33	26	76.5	93	10	US-09-864-761-45734	Sequence 45734, A
34	26	76.5	111	10	US-09-925-299-790	Sequence 790, App
35	26	76.5	139	8	US-08-818-581B-11	Sequence 11, Appl
36	26	76.5	197	10	US-09-811-284-197	Sequence 197, App
37	26	76.5	242	8	US-08-818-581B-9	Sequence 9, Appl1
38	26	76.5	245	8	US-08-818-581B-13	Sequence 13, Appl
39	26	76.5	245	9	US-09-970-989-4	Sequence 4, Appl1
40	26	76.5	253	9	US-09-970-989-9	Sequence 9, Appl1
41	26	76.5	253	9	US-09-895-913A-130	Sequence 130, App
42	26	76.5	263	9	US-09-860-670-115	Sequence 115, App
43	26	76.5	337	9	US-09-828-478-5	Sequence 5, Appl1
44	26	76.5	337	10	US-09-866-230-8	Sequence 8, Appl1
45	26	76.5	343	10	US-09-815-242-11887	Sequence 11887, A

ALIGNMENTS

RESULT 1
US-09-789-561-92
; Sequence 92, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043p1
; CURRENT APPLICATION NUMBER: US/09/789, 561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152, 317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152, 315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (143)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-789-561-92

Query Match 85.3%; Score 29; DB 10; Length 179;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IQIWI 6
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DB 86 INIWI 91

RESULT 2
US-09-789-561-169
; Sequence 169, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:

APPLICANT: N1 et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: P2043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 169
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (225)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
09-789-561-169

Query Match
Best Local Similarity 85.3%; Score 29; DB 10; Length 261;
Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IOIWF 6
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Db 168 IOIWF 173

RESULT 3
US-09-864-761-47624
Sequence 47624, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemlica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47624
LENGTH: 82
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011236.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P08578, EVALU2 2.00e-16
OTHER INFORMATION: EST_HUMAN HIT: BF680487.1, EVALU2 6.00e-31
US-09-864-761-47624

Query Match
Best Local Similarity 82.4%; Score 28; DB 10; Length 82;
Pred. No. 1.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IOIWF 6
|:|:|:
Db 54 IOIWF 59

RESULT 4
US-09-736-457-331
Sequence 331, Application US/09736457
Patent No. US20020168637A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darlick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 331
LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
US-09-736-457-331

Query Match
Best Local Similarity 82.4%; Score 28; DB 9; Length 92;
Pred. No. 1.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IOIWF 6
|:|:|:
Db 31 IOIWF 36

RESULT 5
US-09-902-941-331
; Sequence 331, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-331

Query Match 82.4%; Score 28; DB 9; Length 92;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
||:|:
DB 31 IOVWLX 36

RESULT 6
US-09-849-626-331
; Sequence 331, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tonglong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-331

Query Match 82.4%; Score 28; DB 9; Length 92;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
||:|:
DB 31 IOVWLX 36

RESULT 7

US-09-925-300-1436
; Sequence 1436, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1436
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1436

Query Match 82.4%; Score 28; DB 10; Length 95;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IOIWF 6
||:|:
DB 34 IOVWLX 39

RESULT 8
US-09-815-242-5172
; Sequence 5172, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5172
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5172

Query Match 82.4%; Score 28; DB 10; Length 228;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
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Db 198 VKWIF 203

RESULT 9
US-09-741-669-319
; Sequence 319, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; FILE REFERENCE: ELITRA.009A
; CURRENT FILING DATE: 2000-12-19
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-319

Query Match 82.4%; Score 28; DB 10; Length 233;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
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Db 198 VKWIF 203

RESULT 10
US-09-912-020-386
; Sequence 386, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; FILE REFERENCE: ELITRA.001DV1
; CURRENT FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 386
; LENGTH: 233
; TYPE: PRT
; ORGANISM: E. coli
US-09-912-020-386

Query Match 82.4%; Score 28; DB 10; Length 233;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
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Db 198 VKWIF 203

RESULT 11
US-09-815-242-10353
; Sequence 10353, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10353
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10353

Query Match 82.4%; Score 28; DB 10; Length 233;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQIWF 6
:::||||

Db 198 VKWIF 203

RESULT 12
US-09-815-242-13969
; Sequence 13969, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13969
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Salmonella typhi
; 09-815-242-13969
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Query Match      82.4%; Score 28; DB 10; Length 233;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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OY      1 IQIWIIF 6
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Db      198 VKWVIF 203
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RESULT 13
US-09-815-242-11592
; Sequence 11592, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11592
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; 09-815-242-11592
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Query Match      82.4%; Score 28; DB 10; Length 234;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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OY      1 IQIWIIF 6
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Db      198 VKWVIF 203
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RESULT 14
US-09-815-242-11103
; Sequence 11103, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11103
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
; 09-815-242-11103
```

```
Query Match      82.4%; Score 28; DB 10; Length 235;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 IQIWIIF 6
       ::::|||
Db      198 VKWVIF 203
```

```

RESULT 15
US-09-738-626-3652
; Sequence 3652, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: AMDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIICO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
```

; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 3652
 ; LENGTH: 293
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-3652

Query Match 82.4%; Score 28; DB 9; Length 293;
 Best Local Similarity 50.0%; Pred. No. 3.9e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 IQIWF 6
 :|:|:|
 89 LQIWL 94

Search completed: January 3, 2003, 15:52:06
 Job time : 4.77273 secs

PT New ligands for prion proteins, useful for detection or removal or
PT prions and for treating prion-associated diseases, recognize a specific
PT octapeptide motif -
XX
XX
PS Claim 16; Page 34; 47pp; English.
XX
CC The invention relates to a ligand of less than 6 kD that binds to a
CC polypeptide containing the sequence GLYTYRGLYGLINPROHISGLYGLY (A) or an
CC analogue that is the retro-inverso isomer of (A). The sequence A is
CC an octapeptide motif from the prion protein (Prp). The ligands are
CC identified by binding assays with the peptide (A) or peptides containing
CC (A). The ligands are used for detecting prion proteins (or prions) in
CC biological or environmental samples, e.g. for diagnosis, also for
CC removing them from samples, for treating or retarding development of
CC prion-associated diseases, especially Creutzfeldt-Jakob diseases (in
CC iatrogenic, new variant, familial or sporadic forms), but also
CC Gerstmann-Strausler-Scheinker disease, fatal familial insomnia,
CC scrapie, bovine or feline spongiform encephalopathy, transmissible mink
CC or exotic ungulate encephalopathy, or chronic wasting disease. The
CC present sequence is a ligand of the invention.

Sequence 6 AA:

Query Match 100.0%; Score 38; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
| | | | |
DB 1 WLWVIA 6

RESULT 2
ABBA47793
ID ABBA47793 standard; protein; 371 AA.

ABBA47793:

05-FEB-2002 (first entry)

Listeria monocytogenes protein #497.

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.

Listeria monocytogenes.

MO200177335-A2.

18-OCT-2001.

11-APR-2001; 2001MO-FR01118.

11-APR-2000; 2000FR-0004629.

(INSP) INST PASTEUR.

Buchrieser C, Frangoul L, Couve E, Rusnlok C, Fsihi H, Dehoux P,
PI Dussanget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kieft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Chardit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablo B, Mehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;

WPI: 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides -

Claim 6; SEQ ID No 498; 192pp; French.

XX
XX The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and other organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.

Sequence 371 AA:

Query Match 100.0%; Score 38; DB 23; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
| | | | |
DB 313 WLWVIA 318

RESULT 3
AAG89817
ID AAG89817 standard; protein; 230 AA.

AAG89817:

26-SEP-2001 (first entry)

C glutamicum protein fragment SEQ ID NO: 3571.

Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KW organic acid synthesis.

Corynebacterium glutamicum.

EP1108790-A2.

20-JUN-2001.

18-DEC-2000; 2000EP-0127688.

16-DEC-1999; 99JP-0377484.

07-APR-2000; 2000JP-0159162.

03-AUG-2000; 2000JP-0280988.

(KYOW) KYOWA HAKKO KOGYO KK.

WPI: 2001-376931/40.

N-PSDB; AAH65036.

Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT -

Claim 17; SEQ ID NO: 3571; 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from corynebacterium bacterium, and identifying a homologue of a gene derived
 CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.

CC Sequence 230 AA:

Query Match 97.4%; Score 37; DB 22; Length 230;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 WLWIA 6
 11:111
 170 WLWIA 175

RESULT 4
 AAB76811
 ID AAB76811 standard; Protein: 230 AA.

AC AAB76811;

DT 11-APR-2001 (first entry)

DE Corynebacterium glutamicum MCT protein SEQ ID NO:604.

XX Corynebacterium glutamicum. brevibacterium lactofermentum; MCT;
 KW membrane construction and membrane transport protein; petrioleum spill;
 KW hydrocarbon degradation; gram positive aerobic bacterium; marker;
 KW identification; microorganism; fine chemical production; transformation;
 KW genome mapping; genetic engineering.

XX Corynebacterium glutamicum.

PN WO200100805-A2.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-IB00926.

XX 25-JUN-1999; 99US-0141031.

PR 08-JUL-1999; 99DE-1031454.

PR 08-JUL-1999; 99DE-1031478.

PR 08-JUL-1999; 99DE-1031563.

PR 09-JUL-1999; 99DE-1032122.

PR 09-JUL-1999; 99DE-1032124.

PR 09-JUL-1999; 99DE-1032125.

PR 09-JUL-1999; 99DE-1032128.

PR 09-JUL-1999; 99DE-1032180.

PR 09-JUL-1999; 99DE-1032182.

PR 09-JUL-1999; 99DE-1032190.

PR 09-JUL-1999; 99DE-1032191.

PR 09-JUL-1999; 99DE-1032209.

PR 09-JUL-1999; 99DE-1032212.

PR 09-JUL-1999; 99DE-1032227.

PR 09-JUL-1999; 99DE-1032228.

PR 09-JUL-1999; 99DE-1032229.

PR 09-JUL-1999; 99DE-1032230.

PR 14-JUL-1999; 99DE-1032927.

PR 14-JUL-1999; 99DE-1033005.

PR 14-JUL-1999; 99DE-1033006.

PR 27-AUG-1999; 99DE-1040764.

PR 27-AUG-1999; 99DE-1040765.

PR 27-AUG-1999; 99DE-1040766.

PR 27-AUG-1999; 99DE-1040830.

PR 27-AUG-1999; 99DE-1040831.

PR 27-AUG-1999; 99DE-1040832.
 PR 27-AUG-1999; 99DE-1040833.
 PR 31-AUG-1999; 99DE-1041378.
 PR 31-AUG-1999; 99DE-1041379.
 PR 31-AUG-1999; 99DE-1041395.
 PR 03-SEP-1999; 99DE-1042077.
 PR 03-SEP-1999; 99DE-1042078.
 PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042088.

XX (BADI) BASF AG.

XX Pompejus M, Kroege B, Schroeder H, Zelder O, Haberhauer G;

XX WPI: 2001-071486/08.

DR N-PSDB: AAF68044.

XX

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PS Claim 20; Page 1012; 1119pp; English.

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Query Match 97.4%; Score 37; DB 22; Length 230;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWIA 6
 11:111
 170 WLWIA 175

DB 170 WLWIA 175

XX 25-JUN-1999; 99US-0141031.

PR 08-JUL-1999; 99DE-1031454.

PR 08-JUL-1999; 99DE-1031478.

PR 08-JUL-1999; 99DE-1031563.

PR 09-JUL-1999; 99DE-1032122.

PR 09-JUL-1999; 99DE-1032124.

PR 09-JUL-1999; 99DE-1032125.

PR 09-JUL-1999; 99DE-1032128.

PR 09-JUL-1999; 99DE-1032180.

PR 09-JUL-1999; 99DE-1032182.

PR 09-JUL-1999; 99DE-1032190.

PR 09-JUL-1999; 99DE-1032191.

PR 09-JUL-1999; 99DE-1032209.

PR 09-JUL-1999; 99DE-1032212.

PR 09-JUL-1999; 99DE-1032227.

PR 09-JUL-1999; 99DE-1032228.

PR 09-JUL-1999; 99DE-1032229.

PR 09-JUL-1999; 99DE-1032230.

PR 14-JUL-1999; 99DE-1032927.

PR 14-JUL-1999; 99DE-1033005.

PR 14-JUL-1999; 99DE-1033006.

PR 27-AUG-1999; 99DE-1040764.

PR 27-AUG-1999; 99DE-1040765.

PR 27-AUG-1999; 99DE-1040766.

PR 27-AUG-1999; 99DE-1040830.

PR 27-AUG-1999; 99DE-1040831.

RESULT 5
 AAU47680
 ID AAU47680 standard; Protein: 70 AA.

AC AAU47680;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #8576.

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SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

PA (CORI-) CORIXA CORP.

XX Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A:
PI L'maisonneuve J, Zhang Y, Jen S, Carter D:

XX WPI: 2001-616774/71.
DR N-PSDB: AAS59539.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -

PS Example 1: SEQ ID No 8875; 1069pp; English.

XX Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 70 AA:

Query Match 92.1%; Score 35; DB 22; Length 70;
Best Local Similarity 83.3%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
I:|||||
Db 26 WVWVIA 31

RESULT 6

ABP27890 ABP27890 standard; Protein: 241 AA.

ABP27890;

XX 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 4956.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus agalactiae.

OS

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

XX 27-OCT-2000; 2000GB-0026333.

XX 24-NOV-2000; 2000GB-0028727.

XX 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C:
PI Tettelin H,

XX WPI: 2002-352536/38.
DR N-PSDB: ABN68521.

XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -

PS Claim 1: Page 3656; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5403 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 241 AA:

Query Match 92.1%; Score 35; DB 23; Length 241;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
I:|||||
Db 168 WLWVIA 173

RESULT 7

ABG68706 ABG68706 standard; Protein: 49 AA.

ABG68706;

XX 07-OCT-2002 (first entry)

XX Human prostate specific protein DEX0293_75.

XX Human; prostate specific nucleic acid; PSNA; prostate cancer; PSP;
KW prostate specific protein; cytostatic; non-cancerous prostate disease;
KW gene therapy; cancer; immunostimulant; vaccine.

OS Homo sapiens.

XX WO200255735-A2.

XX 18-JUL-2002.

XX 27-NOV-2001; 2001WO-US44363.

XX 27-NOV-2000; 2000US-253176P.

XX (DIAD-) DIADEXUS INC.

XX Salceda S, Macina RA, Recipon H, Caffarely R, Ali S, Sun Y;

XX Liu C, Chen S;

XX WPI: 2002-557831/59.

DR N-PSDB: ABK97583.
XX New prostate specific genes, useful for treating or diagnosing cancer,
PT or useful as vaccines for treating cancer, particularly prostate
PT cancer, in a patient
XX
PS Claim 11: Page 192; 212pp; English.
XX
CC The invention relates to a new isolated prostate-specific nucleic acid
CC (PSNA) molecule comprising the cDNA sequences appearing as ABK97574-
CC ABK97642 which encode prostate specific proteins appearing as
CC ABG68701-ABG68746, or a sequence hybridizing to a PSNA or which has 60%
CC sequence homology with a PSNA. Also included are a method of determining
CC the presence of a PSNA in a sample, a vector comprising the PSNA,
CC a host cell comprising the vector, producing the polypeptide encoded by
CC the PSNA, a method of determining the presence of a PSP in a sample,
CC diagnosing and monitoring the presence and metastases of prostate cancer
CC in a patient, a kit for detecting a risk of cancer or presence of cancer
CC in a patient (the kit comprising a means for determining the presence of
CC the PSNA or PSP in a sample of a patient) and a vaccine comprising the
CC polypeptide or the nucleic acid encoding the polypeptide. The PSNA, PSP
CC and anti-PSP antibody are useful for diagnosing and treating cancer in a
CC patient (e.g. by gene therapy). The nucleic acid molecule and polypeptide
CC are also useful as vaccines for treating cancer, particularly prostate
CC cancer and non-cancerous prostate diseases. The present sequence is
CC a PSP of the invention.
XX
SQ Sequence 49 AA;

Query Match 89.5%; Score 34; DB 23; Length 49;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVTA 6
1:11:1
Db 8 WVWVWA 13

RESULT 8
AAM86002
ID AAM86002 standard; Protein; 80 AA.
XX
AC AAM86002;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:13595.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0188874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.

PR	01-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	08-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249219.
PR	17-NOV-2000;	2000US-0249220.
PR	17-NOV-2000;	2000US-0249221.
PR	17-NOV-2000;	2000US-0249222.
PR	17-NOV-2000;	2000US-0249223.
PR	17-NOV-2000;	2000US-0249224.
PR	17-NOV-2000;	2000US-0249225.
PR	17-NOV-2000;	2000US-0249226.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249267.
PR	17-NOV-2000;	2000US-0249269.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
 X1
 P1 Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI: 2001-483426/52.
 DR N-PSDB; AAK58783.
 DR
 XX
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS
 XX
 XX
 Claim 11: SEQ ID NO 13595; 3071bp + Sequence Listing: English.
 XX
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAM621170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting

CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (1) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AA864703
CC to AA87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AA54492 to AA84950 and AA882169
CC represent sequences used in the exemplification of the present invention.
XX
XX
Sequence 80 AA:

Query Match	89.5%	Score 34;	DB 22;	Length 80;
Best Local Similarity	66.7%;	Pred. No. 1.3e+02;		
Matches	4;	Conservative	2;	Mismatches 0;
			Indels	0;
			Gaps	0

Qy	1 WLVNIA 6
	11:1:1
Db	61 WLVNVA 66

RESULT 9
AAU32492
ID AAU32492 standard; Protein; 162 AA

DT	18-DEC-2001	(first entry)
XX		
DE	Novel human secreted protein #2983	

Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS	Homo sapiens.
XX	
PN	W0200179449-A2

PD	25-OCT-2001.
XX	
PF	16-APR-2001; 2001WO-US08656

PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;
WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 XX Claim 20; Page 623; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate hematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AA029510-AAU3304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.

SQ Sequence 162 AA;

Query Match 89.5%; Score 34; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVI 5
 I I I I I
 DB 16 WLWVI 20

RESULT 10
 AAU57493
 ID AAU57493 standard; Protein; 235 AA.
 XX
 AC AAU57493;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DT Propionibacterium acnes immunogenic protein #18389.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertrosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.

XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 DR N-PSDB: AAS59583.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 XX vaccinating against and diagnosing infections, especially useful for
 XX treating acne vulgaris -

XX Example 1; SEQ ID No 18688; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertrosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 235 AA;

Query Match 89.5%; Score 34; DB 22; Length 235;
 Best Local Similarity 83.3%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLWVIA 6
 I I I I I
 DB 182 WLWVIA 167

RESULT 11
 AAU42440
 ID AAU42440 standard; Protein; 288 AA.
 XX
 AC AAU42440;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DT Propionibacterium acnes immunogenic protein #3336.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertrosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.

XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI: 2001-616774/71.
 DR N-PSDB: AAS59517.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 XX vaccinating against and diagnosing infections, especially useful for
 XX treating acne vulgaris -

XX Example 1; SEQ ID No 3635; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertrosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 288 AA;
Query Match 89.5%; Score 34; DB 22; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWVI 5
11111
DB 126 WLWVI 130

RESULT 12
AAU35667
ID AAU35667 standard; Protein: 420 AA.
XX
AC AAU35667;
XX
DT 14-FEB-2002 (first entry)
XX
DE Haemophilus influenzae cellular proliferation protein #308.
XX
NM Antisense: prokaryotic cellular proliferation protein;
XX antibiotic; antibacterial; drug design.
XX
OS Haemophilus influenzae.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
XX 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207272P.
XX 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
XX 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI: 2001-611495/70.
DR N-PSDB: AAS53526.
XX
XX New polynucleotides for the identification and development of
antibiotics, comprise sequences of antisense nucleic acids -
Example 3; Seq ID No 11260; 511pp; English.

PS The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX

SQ Sequence 420 AA;
Query Match 89.5%; Score 34; DB 22; Length 420;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWVI 5
11111
DB 10 WLWVI 14

RESULT 13
AA53418
ID AA53418 standard; Protein: 676 AA.
XX
AC AA53418;
XX
DT 13-SEP-1999 (first entry)
XX
DE Chlamydia pneumoniae cellular envelope protein.
XX
DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
XX vaccine; neutralising epitope.
XX
OS Chlamydia pneumoniae.
XX
PN WO927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-1B01890.
XX
PR 04-NOV-1998; 98US-0107078.
XX 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI: 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae
XX
PT
XX
PS Page 1199-1201; Disclosure; 1912pp; English.

PS AA534584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AA534584-Y35879) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AA534584-Y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX

SQ Sequence 676 AA;
Query Match 89.5%; Score 34; DB 20; Length 676;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWVI 5
11111
DB 481 WLWVI 485

RESULT 14
AAB51390
ID AAB51390 standard; Peptide: 38 AA.
XX

AC AAB51390;
XX
XX 16-FEB-2001 (first entry)
XX
DE Human secreted peptide #5 encoded by cDNA #11.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KM antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KM vulnerability; anticonvulsant; antibacterial; antifungal; antiparasitic;
KM cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KM neurological disease; infection; human; secreted protein.
XX
XX Homo sapiens.
OS
XX WO20058495-A1.
PN
XX 05-OCT-2000.
PD
XX 23-MAR-2000; 2000WO-US07661.
XX
XX 26-MAR-1999; 99US-0126504.
PR 07-JAN-2000; 2000US-0174847.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Ruben SM, Komatsoulis G;
PI
XX WPI: 2000-611720/58.
DR N-PSDB; AAC93320.
XX
XX New nucleic acid molecules encoding 45 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
XX Claim 11; Pages 356-357; 410pp; English.
PS
XX Sequences AAB51380-B51423 represent the amino acid sequences of 45
CC human secreted proteins encoded by the genes AAC93310-C93354. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, diabetes mellitus,
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
XX Sequence 38 AA:
SQ
XX
XX Query Match 86.8%; Score 33; DB 21; Length 38;
XX Best Local Similarity 80.0%; Pred. No. 84;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLWVI 5
DB 16 WLWVW 20

RESULT 15
AA002505
ID AA002505 standard; Protein: 78 AA.
XX
XX AA002505;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
DE Human polypeptide SEQ ID NO 16397.

XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX WO200164835-A2.
PN
XX 07-SEP-2001.
PD
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI: 2001-514838/56.
DR N-PSDB; AA182436.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 20; SEQ ID NO 16397; 1399pp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 78 AA:
SQ
XX
XX Query Match 86.8%; Score 33; DB 22; Length 78;
XX Best Local Similarity 80.0%; Pred. No. 1,8e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WLWVI 5
DB 31 WLWVW 35

Search completed: January 3, 2003, 15:28:43
Job time : 28.5909 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:00 : Search time 9.55455 Seconds
(without alignments)
57.944 Million cell updates/sec

Title: US-09-543-188A-27
Perfect score: 38
Sequence: 1 WLWVIA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Reached: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	371	2 AE1190	probable membrane
2	38	100.0	371	2 AE1548	probable membrane
3	37	97.4	719	2 B95325	conserved hypotet
4	35	92.1	651	2 AP2493	hypothetical prote
5	35	92.1	468	2 AD0521	probable symporter
6	35	92.1	536	2 T20736	hypothetical prote
7	35	92.1	565	2 S73854	hypothetical prote
8	35	92.1	585	2 T19814	hypothetical prote
9	34	89.5	285	2 E70473	phosphate transpor
10	34	89.5	318	2 G72310	conserved hypotet
11	34	89.5	420	2 A64132	acylttransferase ho
12	34	89.5	420	2 A64132	hypothetical prote
13	34	89.5	587	2 C85044	hypothetical prote
14	34	89.5	703	2 H72034	hypothetical prote
15	34	89.5	703	2 H85888	thiol-disulfide int
16	34	89.5	714	2 G81503	thiol-disulfide int
17	34	89.5	1394	2 S66876	ATP-dependent tran
18	33	86.8	164	2 T06913	H+-transporting tw
19	33	86.8	172	2 E70057	hypothetical prote
20	33	86.8	179	2 E84126	hypothetical prote
21	33	86.8	188	2 D97260	probable membrane
22	33	86.8	196	2 C84919	hypothetical prote
23	33	86.8	232	2 A95303	probable Aqp2 aqu
24	33	86.8	295	2 AC0499	probable phosphate
25	33	86.8	296	1 BVECP1	phosphate transpor
26	33	86.8	296	2 F91211	hypothetical prote
27	33	86.8	296	2 F86057	hypothetical prote
28	33	86.8	296	2 AD0956	phosphate transpor
29	33	86.8	329	2 E75073	hypothetical prote

30	33	86.8	338	2 E83688	hypothetical prote
31	33	86.8	355	2 C71092	hypothetical prote
32	33	86.8	391	2 C87615	acylttransferase p
33	33	86.8	436	2 T36706	hypothetical prote
34	33	86.8	527	2 A82431	sensor protein Unp
35	33	86.8	594	2 T31824	hypothetical prote
36	33	86.8	594	2 F82895	hypothetical prote
37	33	86.8	638	2 T24676	hypothetical prote
38	33	86.8	692	2 C81653	probable thiol-dis
39	33	86.8	692	2 H71494	probable thiol-dis
40	33	86.8	699	2 H87275	thio-disulfide int
41	33	86.8	735	2 A83006	hypothetical prote
42	33	86.8	815	2 E83294	probable acyl-CoA
43	33	86.8	1411	2 S48442	PDR1 protein - ye
44	32	84.2	40	2 S08038	hypothetical prote
45	32	84.2	170	2 E75017	tRNA intron endonu

ALIGNMENTS

RESULT 1
AE1190
probable membrane protein lmo0925 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1190
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-371 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99003.1; PID:g16410327; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0925

Query Match 100.0%; Score 38; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
Db 313 WLWVIA 318

RESULT 2
AE1548
probable membrane protein lmo0925 [imported] - Listeria innocua (strain Clp11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1548
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1548
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-371 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96157.1; PID:g16413373; GSPDB:GN00178
A:Experimental source: strain Clp11262

C:Genetics:
A:Gene: 11n0925

Query Match 100.0%; Score 38; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
|||||
DB 313 WLWVIA 318

RESULT 3
B95325

conserved hypothetical protein Sma0937 [imported] - *Sinorhizobium meliloti* (strain 1021)
C:Species: *Sinorhizobium meliloti*
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: B95325
R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
R:Barrett, M.J.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
PCC. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: B95325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-719 <KUR>
A:Cross-references: GB:AE006469; PIDN:AK65164.1; PID:g14523607; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Flman, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P.; Chalm, P.; Cowley, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeJaure,
hepault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0937
A:Genome: plasmid

Query Match 97.4%; Score 37; DB 2; Length 719;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
|||||
DB 333 WLWVIA 338

RESULT 4
AF2493

hypothetical protein alr7126 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120a1
C:Species: *Nostoc* sp.
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AF2493
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-651 <KUR>
A:Cross-references: GB:BA000020; PIDN:BA878210.1; PID:g17135664; GSPDB:GN00180
C:Genetics:
A:Experimental source: strain PCC 7120

A:Gene: alr7126
A:Genome: plasmid

Query Match 94.7%; Score 36; DB 2; Length 651;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
|||||
DB 369 WLWVIA 374

RESULT 5
AD0521

probable symporter STY0171 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typh
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A:Note: this species has also been called *Salmonella typhi*
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD0521
R:Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fair
S.; Moutle, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se
A:Reference number: AB0502; PMID:11677608
A:Accession: AD0521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-468 <PAR>
A:Cross-references: GB:AL13382; PIDN:CAD01308.1; PID:g16501436; GSPDB:GN00176
C:Genetics:
A:Gene: STY0171
C:Superfamily: melibiose carrier protein

Query Match 92.1%; Score 35; DB 2; Length 468;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
|||||
DB 82 WLWVIA 87

RESULT 6
T20736

hypothetical protein F11A10.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T20736
R:Smyle, R.
submitted to the EMBL Data Library, December 1995
A:Reference number: T20736
A:Accession: T20736
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-536 <WIL>
A:Cross-references: EMBL:568297; PIDN:CAA92595.1; GSPDB:GN000022; CESP:F11A10.5
A:Experimental source: clone F11A10
C:Genetics:
A:Gene: CESP:F11A10.5
A:Map position: 4
A:Introns: 36/1; 74/2; 100/1; 157/1; 237/1; 269/3; 340/2
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F11A10.5

Query Match 92.1%; Score 35; DB 2; Length 536;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
|||||
DB 9 WLWVIA 14

RESULT 7
S73854

hypothetical protein F10_orf565 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C:Accession: S73854
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73854
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-565 <HTM>
A:Cross-references: EMBL:AE000052; GB:U00089; NID:61674223; PIDN:AA96176.1; PID:6167422
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3

Query Match 92.1%; Score 35; DB 2; Length 565;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMTA 6
|||:|
Db 137 WLWMTA 142

RESULT 8
T19814
hypothetical protein C38C6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T19814
R:Baynes, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19182
A:Accession: T19814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-585 <WIL>
A:Cross-references: EMBL:Z93375; PIDN:CAB07562.1; GSPDB:GN00020; CESP:C38C6.2
C:Genetics:
A:Gene: CESP:C38C6.2
A:Map position: 2
A:Insertions: 17/2; 97/2; 218/1; 299/2; 337/1; 372/3; 517/3; 547/3
A:Superfamily: alpha-glucosidase; alpha-amylase core homology

Query Match 92.1%; Score 35; DB 2; Length 585;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMTA 6
|||:|
Db 105 WLWMTA 110

RESULT 9
E70473
phosphate transport system permease Psta - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 26-Aug-1999
C:Accession: E70473
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: E70473
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-285 <AOF>
A:Cross-references: GB:AE000768; NID:92984249; PIDN:AAC07781.1; PID:92984254; GB:AE00065

A:Experimental source: strain VF5
C:Genetics:
A:Gene: psta
C:Superfamily: phoM protein

Query Match 89.5%; Score 34; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMT 5
|||||
Db 35 WLWMT 39

RESULT 10
G72310
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: G72310
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Ginn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72310
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <ARN>
A:Cross-references: GB:AE001760; GB:AE000512; NID:94981510; PIDN:AA036065.1; PID:9498
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0986

Query Match 89.5%; Score 34; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLWMTA 6
|||||
Db 125 WLWMTA 130

RESULT 11
T44870
acylttransferase homolog [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T44870
R:Parkhill, J.; Barrell, B.G.; Rastandream, M.A.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z22863
A:Accession: T44870
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-384 <PAR>
A:Cross-references: EMBL:AL022486; PIDN:CAA18555.1
A:Experimental source: cosmid B1883
C:Genetics:
A:Note: MICB1883.06
C:Superfamily: 4'''-O-acylttransferase

Query Match 89.5%; Score 34; DB 2; Length 384;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMTA 6
|||:|
Db 120 WLWMTA 125

RESULT 12

A64132
amphotropic murine retrovirus receptor homolog - Haemophilus influenzae (strain Rd KM20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: A64132
R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 436-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: A64132
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-420 <TIGR>
A:Cross-references: GB:U32834; GB:I42023; NID:g1574444; PIDN:AAC23248.1; PID:g1574446; T

Query Match 89.5%; Score 34; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WLWMI 5
|||||
Db 10 WLWMI 14

RESULT 13
C85044
hypothetical protein AT4g03490 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: C85044
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: C85044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <STO>
A:Cross-references: GB:NC_001268; NID:g7270672; PIDN:CAB77834.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g03490
A:Map position: 4

Query Match 89.5%; Score 34; DB 2; Length 587;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 WLWMI 6
|||||
Db 312 WLWMI 317

RESULT 14
H72034
thiol-disulfide interchange protein dsbd [imported] - Chlamydomonas reinhardtii (strain C
C:Species: Chlamydomonas reinhardtii
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 28-Jul-2000
C:Accession: H72034
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydomonas reinhardtii and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: H72034
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-703 <ARR>
A:Cross-references: GB:AE001660; GB:AE001363; NID:g4377095; PIDN:AAD18924.1; PID:g4377095
C:Genetics:
A:Gene: dsbd

Query Match 89.5%; Score 34; DB 2; Length 703;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WLWMI 5
|||||
Db 508 WLWMI 512

RESULT 15
H86588
thio-disulfide interchange protein [imported] - Chlamydomonas reinhardtii (strain J138
C:Species: Chlamydomonas reinhardtii
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: H86588
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydomonas reinhardtii J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: H86588
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-703 <STO>
A:Cross-references: GB:BA000008; NID:g8979159; PIDN:BA098994.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: dsbd

Query Match 89.5%; Score 34; DB 2; Length 703;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WLWMI 5
|||||
Db 508 WLWMI 512

Search completed: January 3, 2003, 15:33:20
Job time : 10.9545 secs

FT TRANSMEM 460 480 POTENTIAL.
FT TRANSMEM 482 502 POTENTIAL.
FT TRANSMEM 516 536 POTENTIAL.
SQ SEQUENCE 565 AA: 62560 MW: ACC745543D2184E2 CRC64:

Query Match 92.1%; Score 35; DB 1; Length 565;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
DB 137 WLWVIA 142

RESULT 2

Y986_THEMA STANDARD: PRT: 318 AA.
ID Y986_THEMA
AC Q9X081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TM0986.
GN TM0986.

OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;

RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
R MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Hafit D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 399:323-328(1999).

CC -1- SIMILARITY: STRONG, TO E.COLI YFAT AND P.AERUGINOSA PA4450.
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EMBL: AE001760; AAD36065.1; -

DR TIGR: TM0986; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 318 AA: 36705 MW: 7041AB7510531380 CRC64:

Query Match 89.5%; Score 34; DB 1; Length 318;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLWVIA 6
DB 125 WLWVIA 130

RESULT 3

YG04_HAEIN STANDARD: PRT: 420 AA.
ID YG04_HAEIN
AC P45268;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative phosphate permease HII604.
GN HII604.

OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;

RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
R MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spiggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd."
RL Science 269:496-512(1995).

CC -1- FUNCTION: POTENTIAL TRANSPORTER FOR PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).

CC -1- SIMILARITY: BELONGS TO THE PHO-4 FAMILY OF TRANSPORTERS.

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EMBL: U32834; AAC23248.1; -
DR TIGR: HII604; -
DR InterPro: IPR001204; Phos-transp.
DR Pfam: PF01384; PHO4; 1.

KW Hypothetical protein; Phosphate transport; Transport; Transmembrane;
KW Inner membrane; Complete proteome.

FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 88 108 POTENTIAL.
FT TRANSMEM 112 132 POTENTIAL.
FT TRANSMEM 145 165 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 216 236 POTENTIAL.
FT TRANSMEM 250 270 POTENTIAL.
FT TRANSMEM 300 320 POTENTIAL.
FT TRANSMEM 343 363 POTENTIAL.
FT TRANSMEM 370 390 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
SQ SEQUENCE 420 AA: 44026 MW: 89651207F01D3810 CRC64:

Query Match 89.5%; Score 34; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVI 5
DB 10 WLWVI 14

RESULT 4

ATPX_CYAPA STANDARD: PRT: 164 AA.
ID AXPX_CYAPA
AC P48085;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase B chain (EC 3.6.3.14) (Subunit II).
GN ATPG.
OS Cyanophora paradoxa.
OG Cyanelle.


```

OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
OX NCBI_TaxID=2762;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=LB555 / Pringsheim;
RC Stitewalt V.L., Michalowski C.B., Loeffelhardt W., Bohert H.J.,
RA Bryant D.A.;
RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
RL Plant Mol. Biol. Rep. 13:327-332(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LB555 / Pringsheim;
RA Loeffelhardt W., Stitewalt V.L., Michalowski C.B., Annarella M.,
RA Farley J.Y., Schlachter W.M., Chung S., Newmann-Spallart C.,
RA Steiner J.M., Jakowitsch J., Bohert H.J., Bryant D.A.;
RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
RL (in) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
Schwenmler W. (eds.);
Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
(1997).
CC -1- FUNCTION: THE B'-SUBUNIT IS A DIVERGED AND DUPLICATED FORM OF
CC B FOUND IN PLANTS AND PHOTOSYNTHETIC BACTERIA.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC H(+)(Out).
CC -1- SUBUNIT: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: CYANELLE THYLAKOID MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
CC -----
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CC -----
CC DR EMBL: U30821; AAA81256.1; -
CC DR InterPro: IPR002146; ATPsynth_B/B'sub.
CC DR Pfam: PF00430; ATP-synt_B; 1.
CC KW Hydrogen ion transport; Transmembrane; CF(0); Cyanelle.
CC SQ SEQUENCE 164 AA; 18568 MW; 49ACCE15AF010D7C CRC64;

Query Match 86.8%; Score 33; DB 1; Length 164;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 WLWIA 6
4 WIIWLA 9

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RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
CC -1- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (by similarity).
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. CYSTM SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: A414160; CAC93564.1; -
CC DR InterPro: IPR000515; BPD_transp.
CC DR TIGRFAMS: TIGR00974; 3a0107s02c; 1.
CC DR PROSITE: PS00402; BPD_TRANS_P. INN MEMBR. 1.
CC KW Transport; Phosphate transport; Transmembrane; Inner membrane;
CC Complete proteome.
CC FT TRANSMEM 29
CC FT TRANSMEM 88 110 POTENTIAL.
CC FT TRANSMEM 123 145 POTENTIAL.
CC FT TRANSMEM 150 169 POTENTIAL.
CC FT TRANSMEM 201 223 POTENTIAL.
CC FT TRANSMEM 268 290 POTENTIAL.
CC SQ SEQUENCE 295 AA; 32331 MW; EEB8B558CB2721EA CRC64;

Query Match 86.8%; Score 33; DB 1; Length 295;
Best Local Similarity 80.0%; Pred. No. 77;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVI 5
44 WLWVI 48

RESULT 6
PSTA_ECOLI STANDARD; PRT; 296 AA.
ID PSTA_ECOLI
AC P07654;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphate transport system permease protein pstA.
GN PSTA OR PHOT OR B3726.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85293094; PubMed=2993631;
RA Anemura M., Makino K., Shingawa H., Kobayashi A., Nakata A.;
RT "Nucleotide sequence of the genes involved in phosphate transport and
RT regulation of the phosphate regulon in Escherichia coli.";
RL J. Mol. Biol. 184:241-250(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85104705; PubMed=3881386;
RA Surin B.P., Rosenberg H., Cox G.B.;
RT "Phosphate-specific transport system of Escherichia coli: nucleotide
RT sequence and gene-polypeptide relationships.";
RL J. Bacteriol. 161:189-198(1985).
RN [3]

```

RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-93315143; PubMed-7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
genome: organizational symmetry around the origin of replication.";
RL Genomics 16:551-561(1993).
RN [4]
RP MUTAGENESIS.
RX MEDLINE-93077562; PubMed-1447208;
RA Webb D.C., Rosenberg H., Cox G.B.;
RT "Mutational analysis of the Escherichia coli phosphate-specific
transport system, a member of the traffic ATPase (or ABC) family of
membrane transporters. A role for proline residues in transmembrane
helices.";
RL J. Biol. Chem. 267:24661-24668(1992).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR PHOSPHATE. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM PERMEASE FAMILY. CYSTM SUBFAMILY.

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CC EMBL; X02723; CA26508.1; -;
DR EMBL; K01992; AAA24380.1; -;
DR EMBL; L10328; AAA62077.1; -;
DR EMBL; AE000449; AAC76749.1; -;
DR PIR; B23311; BVCEPT.
DR EcoGene; EG10782; psta.
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00528; BPD_transp. 1.
DR TrIRPAMS: TIGR00974; 3a0107s02c; 1.
DR PROSITE: PS00402; BPD_TRANS_P_NN_MEMBR. 1.
KW Transport; Phosphate transport; Transmembrane; Inner membrane;
Complete proteome.
FT DOMAIN 1 28 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 29 50 PERIPLASMIC.
FT DOMAIN 51 82 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 83 102 POTENTIAL.
FT DOMAIN 103 126 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 127 146 POTENTIAL.
FT DOMAIN 147 150 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 151 169 POTENTIAL.
FT DOMAIN 170 204 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 205 223 POTENTIAL.
FT DOMAIN 224 266 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 267 286 POTENTIAL.
FT DOMAIN 289 296 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 296 AA: 32321 MW: 32321 MW: BFEADDEC0B9851DC7 CRC64;

Query Match 86.8%; Score 33; DB 1; Length 296;
Best Local Similarity 80.0%; Pred. No. 77;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMI 5
DB 44 WLWMI 48

RESULT 7
ID YAO0_PYRHO STANDARD; PRT; 355 AA.
AC 058728;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PH1000.
GN PH1000.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE-98344137; PubMed-9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.,
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.

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CC EMBL; AP000004; BAA30097.1; -;
DR InterPro: IPR002549; UPF0118.
DR Pfam: PF01594; UPF0118; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 34 54 POTENTIAL.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
FT TRANSMEM 158 178 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
FT TRANSMEM 310 330 POTENTIAL.
SQ SEQUENCE 355 AA: 40179 MW: D0929BBFEA847F39 CRC64;

Query Match 86.8%; Score 33; DB 1; Length 355;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMI 6
DB 258 WLWMI 263

RESULT 8
ID NU2C_NEPOL STANDARD; PRT; 506 AA.
AC 09T107;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADH-plastoquinone oxidoreductase chain 2, chloroplast (EC 1.6.5.3).
GN NDH.
OS Nephroselmis olivacea.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendreales; Chlorodendraceae; Nephroselmis.
OX NCBI_TaxID=31312;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIES-484;
RX MEDLINE-9398694; PubMed-10468594;
RA Turnell M., Otis C., Lemieux C.;

"The complete chloroplast DNA sequence of the green alga *Nephroselmis olivacea*: insights into the architecture of ancestral chloroplast genomes."

Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).

-1- SUBCELLULAR LOCATION: NADH + plastoquinone = NAD(+) + plastoquinol.

-1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.

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DR EMBL: AF137379; AAD54809.1; -.

DR InterPro: IPR001750; Oxidored_q1.

DR Pfam: PF00361; oxidored_q1; 1.

Oxidoreductase; NAD; Plastoquinone; Chloroplast; Transmembrane.

FT	TRANSMEM	15	34	POTENTIAL.
FT	TRANSMEM	41	63	POTENTIAL.
FT	TRANSMEM	85	104	POTENTIAL.
FT	TRANSMEM	117	139	POTENTIAL.
FT	TRANSMEM	172	194	POTENTIAL.
FT	TRANSMEM	215	237	POTENTIAL.
FT	TRANSMEM	247	269	POTENTIAL.
FT	TRANSMEM	282	304	POTENTIAL.
FT	TRANSMEM	338	360	POTENTIAL.
FT	TRANSMEM	380	402	POTENTIAL.
FT	TRANSMEM	417	436	POTENTIAL.
FT	TRANSMEM	469	491	POTENTIAL.
SEQ	SEQUENCE	506 AA;	54338 MW;	073F8705BFFA22A7 CRC64;

Query Match

Best Local Similarity 86.8%; Score 33; DB 1; Length 506;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLVVIA 6

DB 42 WLVVIA 47

RESULT 9

PDRB_YEAST

ID PDRB_YEAST STANDARD; PRT; 1410 AA.

NC P40550; Q03092;

01-FEB-1995 (Rel. 31, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

DE ATP-dependent permease PDR11.

GN PDR11 OR YIL013C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=5288c / AB972;

RA Barrett B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,

RA Churchill C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,

RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,

RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

RA Walsh S.V., Whitehead S.;

RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

RL [2]

RP IDENTIFICATION, AND SEQUENCE OF 1-10.

RC MEDLINE=9555421; PubMed=7629127;

RA Decottignies A., Lambert L., Catly P., Degand H., Epping E.A.,

RA Moye-Rowley W.S., Balzi E., Goffeau A.;

RT Identification and characterization of SNQ2, a new multidrug ATP binding cassette transporter of the yeast plasma membrane.";

RL J. Biol. Chem. 270:18150-18157(1995).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY, PDR5 SUBFAMILY.

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DR EMBL: 238113; CAA86236.1; -.

DR EMBL: 246881; CAA86980.1; -.

DR SGD: S0001275; PDR11.

DR InterPro: IPR003439; ABC_transport.

DR Pfam: PF00005; ABC_tran; 2.

DR ProDom: PD000006; ABC_transporter; 2.

DR PROSITE: PS00211; ABC_TRANSPORTER; 1.

KW ATP-binding; Transmembrane; Glycoprotein; Transport.

FT	INIT MET	0	0	
FT	DOMAIN	1	387	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	388	408	POTENTIAL.
FT	TRANSMEM	418	438	POTENTIAL.
FT	TRANSMEM	471	491	POTENTIAL.
FT	TRANSMEM	494	514	POTENTIAL.
FT	TRANSMEM	524	544	POTENTIAL.
FT	TRANSMEM	636	656	POTENTIAL.
FT	DOMAIN	657	1089	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1090	1110	POTENTIAL.
FT	TRANSMEM	1117	1137	POTENTIAL.
FT	TRANSMEM	1175	1195	POTENTIAL.
FT	TRANSMEM	1204	1224	POTENTIAL.
FT	TRANSMEM	1230	1250	POTENTIAL.
FT	TRANSMEM	1335	1375	POTENTIAL.
FT	DOMAIN	1376	1410	CYTOPLASMIC (POTENTIAL).
FT	NP_BIND	781	788	ATP (POTENTIAL).
FT	DOMAIN	707	712	POLY-SER.
FT	DOMAIN	1045	1048	POLY-LEU.
FT	CARBOHYD	594	594	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1288	1288	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1323	1323	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1345	1345	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	1410 AA;	160405 MW;	93C9399A5CD114C3 CRC64;

Query Match

Best Local Similarity 86.8%; Score 33; DB 1; Length 1410;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLVVIA 6

DB 552 WLVVIA 557

RESULT 10

YPSL_PLEBO

ID YPSL_PLEBO STANDARD; PRT; 40 AA.

AC P15733;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DE Hypoetical 4.6 kDa protein (ORF1).

OS Plectonema boryanum.

OG Plectonema small.

OC Bacteria; Cyanobacteria; Oscillatoriales; Plectonema.

OX NCBI_TaxID=1184;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 27894 / UTEX 581;

RA Wickrema A., Barnum S.R., Jaworski J.G.;

RL Submitted (JAN-1989) to the EMBL/GenBank/DBJ databases.

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CC -----
CC EMBL: X51320; -; NOT_ANNOTATED_CDs.
CC DR PIR: S08038; S08038.
CC KM Hypothetical protein; Plasmid.
CC SQ SEQUENCE 40 AA: 4592 MW: 83D6BFD8296D7D37 CRC64:

Query Match 84.2%; Score 32; DB 1; Length 40;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWMI 5
DB 11 MWMI 15

RESULT 11
MERT_SHEPU STANDARD; PRT; 115 AA.
ID MERT_SHEPU
AC Q54462;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mercuric transport protein (Mercury ion transport protein).
GN MERT.
OS Shewanella putrefaciens (Pseudomonas putrefaciens).
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Shewanella.
CC NCB1_TaxID=24;
CC (1)
CC SEQUENCE FROM N.A.
CC MEDLINE-97309939; PubMed-9167257;
CC RA Osborn A.M., Bruce R.D., Strike P., Ritchie D.A.;
CC "Distribution, diversity and evolution of the bacterial mercury
CC resistance (mer) operon."
CC FEMS Microbiol. Rev. 19:239-262(1997).
CC -1- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
CC FROM THE PERIPLASMIC MERT PROTEIN TO THE MERCURIC REDUCTASE
CC (MERA).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC (BY SIMILARITY).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 249196; CA89054.1; -;
CC DR InterPro: IPR003457; Transprt_Mert.
CC DR Pfam: PF02411; MERT; 1.
CC KM Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid;
CC Transmembrane.
CC KW TRANSMEM 10 30 POTENTIAL.
CC FT TRANSMEM 45 65 POTENTIAL.
CC FT TRANSMEM 92 112 POTENTIAL.
CC FT TRANSMEM 23 23 HG(2+) (BY SIMILARITY).
CC FT METAL 24 24 HG(2+) (BY SIMILARITY).
CC FT METAL 75 75 HG(2+) (BY SIMILARITY).
CC FT METAL 81 81 HG(2+) (BY SIMILARITY).
CC SQ SEQUENCE 115 AA: 12555 MW: C4ADC83CD389074E CRC64:

Query Match 84.2%; Score 32; DB 1; Length 115;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLWMI 6
DB 110 WLWMI 115

RESULT 12
ERD2_PETHY STANDARD; PRT; 215 AA.
ID ERD2_PETHY
AC O92TN2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ER lumen protein retaining receptor (HDEL receptor) (PGP169-12).
GN ERD2.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
CC NCB1_TaxID=4102;
CC (1)
CC SEQUENCE FROM N.A.
CC MEDLINE-20317212; PubMed-10859200;
CC RA Guyon V.N., Astwood J.D., Garner E.C., Dunker A.K., Taylor L.P.;
CC "Isolation and characterization of cDNAs expressed in the early
CC stages of flavonol-induced pollen germination in petunia."
CC Plant Physiol. 123:699-710(2000).
CC -1- FUNCTION: REQUIRED FOR THE RETENTION OF LUMINAL ENDOPLASMIC
CC RETICULUM PROTEINS, DETERMINES THE SPECIFICITY OF THE LUMINAL ER
CC PROTEIN RETENTION SYSTEM. ALSO REQUIRED FOR NORMAL VESICULAR
CC TRAFFIC THROUGH THE GOLGI. THIS RECEPTOR RECOGNIZES H-D-E-L (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC (BY SIMILARITY).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF049922; AAD02548.1; -;
CC DR InterPro: IPR000133; Eretl_receptor.
CC DR Pfam: PF00810; ER_lumen_recept; 1.
CC DR PRINTS: PR00660; ERLUMENR.
CC DR PRODOM: P0005774; Eretl_receptor; 1.
CC DR PROSITE: PS00951; ER_LUMEN_RECEPTOR_1; 1.
CC DR PROSITE: PS00952; ER_LUMEN_RECEPTOR_2; 1.
CC KW Endoplasmic reticulum; Transmembrane; Protein transport; Receptor.
CC FT DOMAIN 1 2 LUMENAL (POTENTIAL).
CC FT TRANSMEM 3 21 POTENTIAL.
CC FT DOMAIN 22 35 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 36 53 POTENTIAL.
CC FT DOMAIN 54 61 LUMENAL (POTENTIAL).
CC FT TRANSMEM 62 82 POTENTIAL.
CC FT DOMAIN 83 98 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 99 112 POTENTIAL.
CC FT DOMAIN 113 119 LUMENAL (POTENTIAL).
CC FT TRANSMEM 120 139 POTENTIAL.
CC FT DOMAIN 140 151 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 152 170 POTENTIAL.
CC FT DOMAIN 171 181 LUMENAL (POTENTIAL).
CC FT TRANSMEM 182 202 POTENTIAL.
CC FT DOMAIN 203 215 CYTOPLASMIC (POTENTIAL).
CC SQ SEQUENCE 215 AA: 25602 MW: 7A6E4FE4F01CF65 CRC64:

Query Match 84.2%; Score 32; DB 1; Length 215;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 181 WITWIA 186

RESULT 13

AOPZ_BRUBA STANDARD: PRT; 228 AA.

AC 09LA79;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Aquaporin 2 (Aquaporin X).

GN AOPZ OR AOPX.

OS Brucella abortus.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Brucellaceae; Brucella.

OX NCBI_TaxID=235;

RN [1]

SEQUENCE FROM N.A.

STRAIN=2308;

MEDLINE=20553188; PubMed=11101683;

Rodriguez M.C., Proger A., Rolland J.-P., Thomas D., Aguero J.,

Delamarque C., Garcia-Lobo J.M.,

"A functional water channel protein in the pathogenic bacterium

Brucella abortus."

RT Microbiology 146:3251-3257(2000).

CC -1- FUNCTION: Transport of water across the membrane. Possibly

involved in the adaptation to variation in intravacuolar pH or

osmolality.

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

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CC EMBL: AF148066; AAF3105.1; -

DR HSSP: P29972; 1H61.

DR InterPro: IPR000425; MIP_family.

DR Pfam: PF00230; MIP_1.

DR PRINTS: PR00783; MINTRENSICP.

DR ProDom: PD000295; MIP_family; 1.

DR TIGRFAMs: TIGR00861; MIP; 1.

DR PROSITE: PS00221; MIP; 1.

CC TRANSPORT; Transmembrane; Inner membrane; Repeat.

FT TRANSMEM 7 29

FT TRANSMEM 34 56

FT TRANSMEM 81 103

FT TRANSMEM 127 149

FT TRANSMEM 154 176

FT TRANSMEM 203 225

FT REPEAT 63 65

FT REPEAT 184 186

FT SITE 20 20

FT INVOLVED IN TETRAMERIZATION OR STABILITY

FT OF THE TETRAMER (BY SIMILARITY).

FT POLY-ALA.

FT DOMAIN 92 97

FT SEQUENCE 228 AA; 23145 MW; 23664C39E4DD44A CRC64;

Query Match

Best Local Similarity 84.2%; Score 32; DB 1; Length 228;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 204 WLEFWA 209

RESULT 14

AOPZ_BRUME STANDARD: PRT; 228 AA.

AC 09L772;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Aquaporin 2.

GN AOPZ OR BME10070.

OS Brucella melitensis.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Brucellaceae; Brucella.

OX NCBI_TaxID=29459;

RN [1]

SEQUENCE FROM N.A.

STRAIN=133;

RA Hernandez-Castro R., Verdugo-Rodriguez A., Gutierrez-Pabello J.A.,

Suarez-Guemes F.;

"Cloning and nucleotide sequence of aquaporin gene of Brucella

melitensis."

RT Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.

RN [2]

SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688;

RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Moser T.,

Ivanova N., Anderson I., Bhattacharya A., Lykdis A., Resnik G.,

Tjablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyriades N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen

Brucella melitensis."

RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

CC -1- FUNCTION: Transport of water across the membrane. Possibly

involved in the adaptation to variation in intravacuolar pH or

osmolality (By similarity).

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

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CC EMBL: AF26624; AAF36396.1; -

DR HSSP: P29972; 1H61.

DR InterPro: IPR000425; MIP_family.

DR Pfam: PF00230; MIP_1.

DR PRINTS: PR00783; MINTRENSICP.

DR ProDom: PD000295; MIP_family; 1.

DR TIGRFAMs: TIGR00861; MIP; 1.

DR PROSITE: PS00221; MIP; 1.

CC TRANSPORT; Transmembrane; Inner membrane; Repeat; Complete proteome.

FT TRANSMEM 7 29

FT TRANSMEM 34 56

FT TRANSMEM 81 103

FT TRANSMEM 127 149

FT TRANSMEM 154 176

FT TRANSMEM 203 225

FT REPEAT 63 65

FT REPEAT 184 186

FT SITE 20 20

FT INVOLVED IN TETRAMERIZATION OR STABILITY

FT OF THE TETRAMER (BY SIMILARITY).

FT POLY-ALA.

FT DOMAIN 92 97

FT SEQUENCE 228 AA; 23189 MW; 64282C39E4DD4109 CRC64;

Query Match

Best Local Similarity 84.2%; Score 32; DB 1; Length 228;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLWVA 6

DB 204 WLFWA 209

RESULT 15

Y836_AQUAE

ID Y836_AQUAE STANDARD; PRT; 232 AA.

AC 067008; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

GN Hypothetical protein AQ_836.

OS Aquifex aeolicus.

OC Bacteria; Aquificae; Aquificales; Aquificaceae;

OC Aquifex.

NCBI_TaxID=63363;

SEQUENCE FROM N.A.

STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,

RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,

RT "The complete genome of the hyperthermophilic bacterium Aquifex

aeolicus."

RL Nature 392:353-358(1998).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

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CC or send an email to license@sib-sib.ch).

CC -----

DR EMBL: AE00709; AAC06970.1; -

KW Hypothetical protein; Transmembrane; Complete proteome.

FT TRANSMEM 4 24 POTENTIAL.

FT TRANSMEM 42 62 POTENTIAL.

FT TRANSMEM 100 120 POTENTIAL.

FT TRANSMEM 145 165 POTENTIAL.

FT TRANSMEM 171 191 POTENTIAL.

SQ SEQUENCE 232 AA: 26317 MW: B934B56FEA35B183 CRC64;

Query Match

Best Local Similarity 84.2%; Score 32; DB 1; Length 232;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVA 5

DB 183 WLWVA 187

Search completed: January 3, 2003, 15:29:24

Job time : 6.18182 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:24:35 ; Search time 20.3182 seconds
(without alignments)
60.846 Million cell updates/sec

Title: US-09-543-188a-27

Perfect score: 38
Sequence: 1 MLWVIA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	371	16	Q92D92
2	38	100.0	371	16	Q8Y8H8
3	38	100.0	598	16	Q8Y063
4	37	97.4	719	16	Q92ZM9
5	36	94.7	438	16	Q8XPT4
6	36	94.7	651	16	Q8YLI2
7	35	92.1	234	16	Q8CK00
8	35	92.1	358	5	Q967S2
9	35	92.1	418	16	Q8Y0V2
10	35	92.1	463	5	Q967S1
11	35	92.1	468	16	Q8Z9F2
12	35	92.1	468	16	Q9L4I1
13	35	92.1	536	5	Q19337
14	35	92.1	555	5	Q906X2
15	35	92.1	556	5	Q967S3
16	35	92.1	585	5	O45298

17	34	89.5	61	2	Q9AML5	Q9aml5 edwardsiell
18	34	89.5	162	8	Q94ZA9	Q94za9 lepidapedon
19	34	89.5	162	8	Q94Z92	Q94z92 lepidapedon
20	34	89.5	168	9	Q8SD14	Q8sd14 pseudomonas
21	34	89.5	247	11	Q8RI89	Q8ri89 mus musculu
22	34	89.5	285	16	Q67817	Q67817 aquilex aeo
23	34	89.5	296	2	Q32486	Q32486 enterobacte
24	34	89.5	316	2	Q07450	Q07450 alcaligenes
25	34	89.5	326	17	Q8U1U9	Q8u1u9 pyrococcus
26	34	89.5	384	16	Q69496	Q69496 mycobacteri
27	34	89.5	453	3	Q02922	Q02922 saccharomyc
28	34	89.5	587	10	Q9ZT77	Q9zt77 arabidopsis
29	34	89.5	602	5	Q8SMH6	Q8smh6 encephalito
30	34	89.5	703	16	Q9Z7C0	Q9z7c0 chlamydia p
31	34	89.5	714	16	Q9K1S6	Q9k1s6 chlamydia p
32	34	89.5	1006	3	Q07324	Q07324 saccharomyc
33	34	89.5	1040	3	Q94147	Q94147 saccharomyc
34	34	89.5	1394	3	Q08409	Q08409 saccharomyc
35	33	86.8	162	8	Q94ZB0	Q94zb0 lepidapedon
36	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
37	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
38	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
39	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
40	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
41	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
42	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
43	33	86.8	162	8	Q94ZAT	Q94zat lepidapedon
44	33	86.8	170	17	Q8U429	Q8u429 prodicistomm
45	33	86.8	171	10	Q9LV89	Q9lv89 pyrococcus

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	371 AA.
ID Q92D92	Q92D92		
AC Q92D92	Q92D92		
DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE Putative membrane protein.			
GN LIN0925.			
OS Listeria innocua.			
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;			
OC Listeriaceae; Listeria.			
OX NCBI_TaxID=1642;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CLIP 11262 / SEROVAR 6A;			
RX PubMed=11679669;			
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,			
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,			
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,			
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,			
RA Ertlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,			
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,			
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,			
RA Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,			
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,			
RA Remmel B., Rose M., Schleuter T., Simoes N., Tierrez A.,			
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,			
RT "Comparative genomics of Listeria species.";			
RL Science 294:849-852(2001).			
DR EMBL: AL596166; CAC96157.1; -.			
DR Listerist; LIN0925;			
KW Hypothetical protein; Complete proteome.			
SO SEQUENCE 371 AA; 41360 MW; 4E94A30E917C242 CRC64;			
Query Match	100.0%;	Score 38;	DB 16; Length 371;
Best Local Similarity	100.0%;	Pred. No. 89;	
Matches	6;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
 |||||
 Db 313 WLWVIA 318

RESULT 2

O8Y8H8

AC 08Y8H8 PRELIMINARY: PRT: 371 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

GN LMO0925.

OS Listeria monocytogenes.

OC Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Listeriaceae; Listeria.

OX NCBI_TaxID=1639;

RN [1]

SEQUENCE FROM N.A.

MEDLINE-21537279; PubMed11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,

RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Ertlan K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordisk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

RT "Comparative genomics of Listeria species."

RL Science 294:849-852(2001).

DR EMBL: AL591977; CAC99003.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 371 AA; 41252 MW; 54E7E86545CA62E CRC64;

Query Match 100.0%; Score 38; DB 16; Length 371;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
 |||||
 Db 313 WLWVIA 318

RESULT 3

O8Y063

AC 08Y063 PRELIMINARY: PRT: 598 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

GN RSC181 OR RS05713.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OX NCBI_TaxID=305;

RN [1]

SEQUENCE FROM N.A.

MEDLINE-21681879; PubMed11823852;

RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

RA Chandier M., Choise N., Claudel-Renard C., Cunac S., Demange N.,

RA Gaspin C., Layle M., Moisan A., Robert C., Saurin W., Schlex F.,

RA Sigler P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weissenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).
 DR EMBL: AL646063; CAD14883.1; -.
 KW Complete proteome.
 SQ SEQUENCE 598 AA; 66422 MW; 8798BC65EA5C6646 CRC64;

Query Match 100.0%; Score 38; DB 16; Length 598;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
 |||||
 Db 393 WLWVIA 398

RESULT 4

O92ZH9

AC 092ZH9 PRELIMINARY: PRT: 719 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN RA0506 OR SMA0937.

OS Rhizobium meliloti (Sinorhizobium meliloti).

OC Plasmid pSymA (megaplasmid 1).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Sinorhizobium.

OX NCBI_TaxID=382;

RN [1]

SEQUENCE FROM N.A.

MEDLINE-21396509; PubMed11481432;

RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

RA Barloy-Hubler F., Bowser L., Capela D., Galburt F., Gouzy J.,

RA Gurjal M., Hong A., Huzar L., Hyman R.W., Kahn D., Kahn M.L.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RT "Nucleotide sequence and predicted functions of the entire

RT Sinorhizobium meliloti pSymA megaplasmid."

RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).

DR EMBL: AE007241; AAK65164.1; -.

DR InterPro: IPR001880; MSion_channel.

DR InterPro: IPR000504; RNA_rec_mot.

DR Pfam: PF00924; MS_channel.1.

DR PROSITE: PS00030; RRM_RNP.1; UNKNOWN.1.

KW Plasmid; Hypothetical protein; Complete proteome.

SQ SEQUENCE 719 AA; 77245 MW; 045DBCB16917B9 CRC64;

Query Match 97.4%; Score 37; DB 16; Length 719;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWVIA 6
 |||||
 Db 333 WLWVIA 338

RESULT 5

O8XPT4

AC 08XPT4 PRELIMINARY: PRT: 438 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE regulator protein (EC 2.7.7.7).

GN RSP1553 OR RS02109.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Plasmid megaplasmid.

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-GM1100;
RX MEDLINE-21681879; PubMed-11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Manjencot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Chouane N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Laye M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siglier P., Trebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*,"
RL Nature 415:497-502(2002).
DR EMBL: AL646085; CAD18704.1; -
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003660; HAMF.
DR InterPro: IPR004359; His_kinA.
DR InterPro: IPR003661; His_kinA.
DR Pfam: PF00672; HAMF; 1.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF00512; signal; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR SMART: SM00387; HATPase_C; 1.
DR SMART: SM00388; HSKA; 1.
DR PROSITE: PS50109; HIS_KIN; 1.
DR Transferrase: Plasmid; Complete proteome.
SQ SEQUENCE 438 AA; 46589 MW; A28879BB7E0B074D CRC64;

Query Match 94.7%; Score 36; DB 16; Length 438;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWVIA 6
Db 155 WLWVIA 160

RESULT 6
Q8YL12 PRELIMINARY; PRT; 651 AA.
AC Q8YL12;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical protein Alr7126.
GN ALR7126.
OS Anabaena sp. (strain PCC 7120).
OC Plasmid PCC7120alpha.
OC Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21595285; PubMed-11759840;
RA Kaneo T., Nakamura Y., Wolk G.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iritiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsuno M., Matsuo A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium *Anabaena* sp. strain PCC 7120,"
RL DNA Res. 8:205-213(2001).
DR EMBL: AF003600; BAB78210.1; -
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 651 AA; 74404 MW; 6AB753997CD2C809 CRC64;

Query Match 94.7%; Score 36; DB 16; Length 651;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWVIA 6
Db 369 WLWVIA 374

RESULT 7
Q9CK00 PRELIMINARY; PRT; 234 AA.
AC Q9CK00;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Hypothetical protein PM188.
GN PM188.
OS Pasteurella multocida
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OC NCBI_TaxID=747;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-Pm70.
RX MEDLINE-21145866; PubMed-11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;
RT "Complete genomic sequence of *Pasteurella multocida* Pm70,"
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL: AF006221; AAK03922.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 234 AA; 26264 MW; 0B31A94DD2AA2F9 CRC64;

Query Match 92.1%; Score 35; DB 16; Length 234;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWVIA 6
Db 180 WLWVIA 185

RESULT 8
Q967S2 PRELIMINARY; PRT; 358 AA.
AC Q967S2;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Nuclear receptor nhr-7B.
GN NHR-7.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota: Metazoa: Nematoda: Chromadorea: Splurrida: Filarioidae;
OC Onchocercidae; Dirofilaria.
OC NCBI_TaxID=6287;
[1]
RP SEQUENCE FROM N.A.
RA Crossgrove K., Laudet V., Maina C.V.;
RT "Dirofilaria immitis encodes dhnr-7, a putative homolog of the
Drosophila ecdysone-regulated E78 gene,"
Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF367207; AAK54128.1; -
DR EMBL: AF367207; AAK54128.1; -
DR InterPro: IPR000536; Hormone_rec_1lg.
DR InterPro: IPR001628; znf_C4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR ProDom: PD000035; znf_C4steroid; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 358 AA; 41669 MW; 2C01ED1D96C86C9E CRC64;

Query Match 92.1%; Score 35; DB 5; Length 358;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWVIA 6
Db 166 WLWVIA 171

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RESULT 9
Q8Y0V2 PRELIMINARY; PRT; 418 AA.
AC 08Y0V2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable integral membrane protease transmembrane protein
DE (EC 3.4.-).
GN RSC0941 OR RS04465.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GM11000;
RC MEDLINE-2161879; PubMed-11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguler P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646061; CAD14643.1; -
DR InterPro: IPR001915; Peptidase_M48.
DR Pfam: PF01435; Peptidase_M48; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 418 AA; 46610 MW; 8ACCD9903C85D52 CRC64;

Query Match
Best Local Similarity 92.1%; Score 35; DB 16; Length 418;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
Db 180 WLWVMA 185

RESULT 10
Q967S1 PRELIMINARY; PRT; 463 AA.
AC 0967S1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Nuclear receptor nhr-7C.
DE NHR-7.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RC Crossgrove K., Laudet V., Maine C.V.;
RT "Dirofilaria immitis encodes dinhr-7, a putative homolog of the
RT Drosophila ecdysone-regulated E78 gene.";
RC Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DE -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DE EMBL: AF367208; AK54129.1; -
DR InterPro: IPR000536; Hormone_rec_119.
DR InterPro: IPR001628; Zn1_C4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF000035; znf_C4steroid; 1.
DR ProDom: PD000035; znf_C4steroid; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 463 AA; 52253 MW; A3430D0FAC35DF8E CRC64;

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Query Match
Best Local Similarity 92.1%; Score 35; DB 5; Length 463;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
Db 360 WLWVIS 365

RESULT 11
Q829F2 PRELIMINARY; PRT; 468 AA.
AC 0829F2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative symporter.
DE SY0171.
GN Salmonella typhi.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CT18;
RC MEDLINE-21534947; PubMed-11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL: AL627265; CAD01308.1; -
DR InterPro: IPR001092; HLH_basic.
DR InterPro: IPR001927; Na/Gal_symp.
DR TIGRfams: TIGR00792; gph; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 468 AA; 52589 MW; 883F0DF78D3A87 CRC64;

Query Match
Best Local Similarity 92.1%; Score 35; DB 16; Length 468;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
Db 82 WLWVIA 87

RESULT 12
Q9L4I1 PRELIMINARY; PRT; 468 AA.
AC 09L4I1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 52.4 kDa protein (Putative permease of the
DE Na+/galactoside symporter family).
DE SY0049.
GN Salmonella typhimurium.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SL1344;
RC Cano D., Casadesus J., Garcia-del Portillo F.;
RT "Characterization of a Salmonella-specific region located between ampe

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RT and arcp genes.";
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Greal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
DR EMBL: AJ242516; CAB8938.1; -;
DR EMBL: AE008700; AAL19113.1; -;
DR InterPro: IPR001927; Na/Gal_symp.
DR TIGRfams: TIGR00792; gph; 1.
PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
HYPOTHETICAL protein; Complete proteome.
SQ SEQUENCE 468 AA; 52443 MW; 5545BA3CB3EAB0B3A CRC64;

Query Match 92.1%; Score 35; DB 16; Length 468;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWITA 6
DB 82 WLWITA 87

RESULT 13
ID 019337 PRELIMINARY; PRT; 536 AA.
AC 019337;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FL1A10.5 protein.
GN FL1A10.5.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; *Caenorhabditis*.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
Smye R.;
Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode *C.elegans*: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z68297; CAA92595.1; -;
SQ SEQUENCE 536 AA; 60611 MW; 0449018148FBC181 CRC64;

Query Match 92.1%; Score 35; DB 5; Length 536;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Nuclear hormone receptor.
OS *Onchocerca volvulus*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; *Onchocerca*.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20058753; PubMed=10593180;
RA Unnasch T.R., Bradley J., Beauchamp J., Tuan R., Kennedy M.W.;
RT "Characterization of a putative nuclear receptor from *Onchocerca*
RT *volvulus*.";
RL Mol. Biochem. Parasitol. 104:259-269(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF170551; AAF06997.1; -;
DR HSSP: P20393; 1A6Y.
DR InterPro: IPR000536; Hormone_rec_119.
DR InterPro: IPR001723; Steroid_receptor.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00398; STRDHORMONER.
DR PRINTS: PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR SMART: SM00430; HOL1; 1.
DR SMART: SM00399; Znf_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 555 AA; 62847 MW; E813CB9F2C94087 CRC64;

Query Match 92.1%; Score 35; DB 5; Length 555;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWITA 6
DB 363 WLWITA 368

RESULT 15
ID 096753 PRELIMINARY; PRT; 556 AA.
AC 096753;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Nuclear receptor nhr-7A.
GN NHR-7.
OS *Dirofilaria immitis* (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; *Dirofilaria*.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
Crossgrove K., Laudet V., Maina C.V.;
RT "Dirofilaria immitis encodes dinhr-7, a putative homolog of the
RT drosophila ecdysone-regulated E78 gene.";
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL: AF367206; AAK54127.1; -;
DR InterPro: IPR000536; Hormone_rec_119.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 556 AA; 63342 MW; 2F7995FAFB5126F CRC64;

Query Match 92.1%; Score 35; DB 5; Length 556;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLWIA 6
|||||:
Db 364 WLWIS 369

Search completed: January 3, 2003, 15:32:04
Job time : 21.3182 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:16 ; Search time 9 seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-543-188a-27

Perfect score: 38

Sequence: 1 MLWIA 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Database: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Dackfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	86.8	362	1	US-08-118-270-16
2	33	86.8	362	5	PCT-US93-08528-16
3	33	86.8	572	6	5200183-5
4	32	84.2	75	4	US-08-469-260A-478
5	32	84.2	139	1	US-08-137-117D-35
6	32	84.2	139	2	US-08-436-717-35
7	32	84.2	266	6	5223610-5
8	32	84.2	269	6	5244657-5
9	32	84.2	269	6	5433945-5
10	32	84.2	837	4	US-09-122-126B-2
11	31	81.6	50	4	US-08-469-260A-534
12	31	81.6	377	4	US-09-316-080-5
13	31	81.6	380	4	US-09-316-080-2
14	31	81.6	438	4	US-08-952-365-2
15	31	81.6	705	2	US-08-663-566A-19
16	31	81.6	705	2	US-08-023-610-19
17	31	81.6	705	2	US-08-288-065A-19
18	31	81.6	705	2	US-08-362-240A-19
19	31	81.6	705	5	PCT-US95-10245-19
20	31	81.6	1162	2	US-08-663-566A-15
21	31	81.6	1162	2	US-08-023-610-15
22	31	81.6	1162	2	US-08-288-065A-15
23	31	81.6	1162	2	US-08-362-240A-15
24	31	81.6	1162	5	PCT-US95-10245-15
25	30	78.9	24	2	US-08-470-419-2
26	30	78.9	24	2	US-08-761-828-2
27	30	78.9	24	2	US-08-290-105-2

28	30	78.9	24	3	US-08-776-949-2	Sequence 2, Appl1
29	30	78.9	24	3	US-08-482-810-2	Sequence 2, Appl1
30	30	78.9	24	4	US-09-027-955-2	Sequence 2, Appl1
31	30	78.9	24	4	US-09-636-805-2	Sequence 2, Appl1
32	30	78.9	24	4	US-09-258-128-2	Sequence 2, Appl1
33	30	78.9	52	2	US-08-470-419-4	Sequence 4, Appl1
34	30	78.9	52	2	US-08-761-828-4	Sequence 4, Appl1
35	30	78.9	52	2	US-08-290-105-4	Sequence 4, Appl1
36	30	78.9	52	3	US-08-776-949-4	Sequence 4, Appl1
37	30	78.9	52	3	US-08-482-810-4	Sequence 4, Appl1
38	30	78.9	52	4	US-09-027-955-4	Sequence 4, Appl1
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41	30	78.9	143	3	US-08-834-033A-12	Sequence 11, Appl1
42	30	78.9	143	3	US-08-834-033A-12	Sequence 11, Appl1
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44	30	78.9	143	4	US-09-363-526-11	Sequence 11, Appl1
45	30	78.9	145	5	PCT-US94-01149-69	Sequence 69, Appl1

ALIGNMENTS

RESULT 1
US-08-118-270-16
; Sequence 16, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-118-270-16
Query Match 86.8%; Score 33; DB 1; Length 362;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWIA 5

Db 120 WLWV 124

||||

RESULT 2

PCT-US93-08528-16

Sequence 16, Application PC/TUS9308528

GENERAL INFORMATION:

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY-2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 362 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US93-08528-16

Query Match Best Local Similarity 86.8%; Score 33; DB 5; Length 362;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWV 5

Db 120 WLWV 124

RESULT 3

5200183-5

Patent No. 5200183

APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN

TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES

NUMBER OF SEQUENCES: 22

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/537,426

FILING DATE: 12-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 504,635

FILING DATE: 04-APR-1990

APPLICATION NUMBER: 122,410

FILING DATE: 19-NOV-1987

SEQ ID NO: 5

LENGTH: 572

5200183-5

Query Match Best Local Similarity 86.8%; Score 33; DB 6; Length 572;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWV 5

Db 107 WLWV 111

RESULT 4

US-08-469-260A-478

Sequence 478, Application US/08469260A

Patent No. 6451578

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS

APPLICANT: TAMI J. PILOT-MATIAS

APPLICANT: GEORGE J. DAWSON

APPLICANT: GEORGE G. SCHLAUDER

APPLICANT: SURESH M. DESAI

APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUEHROFF

APPLICANT: JAMES C. ERKER

APPLICANT: SHERI L. BUIK

APPLICANT: ISA K. MUSHAMMAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,260A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: POREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-938-2623

TELEFAX: 708-937-6365

INFORMATION FOR SEQ ID NO: 478:

SEQUENCE CHARACTERISTICS:

LENGTH: 75 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-469-260A-478

Query Match Best Local Similarity 84.2%; Score 32; DB 4; Length 75;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLWV 6

Db 2 WLWV 7

RESULT 5

US-08-137-117D-35

Sequence 35, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-35

Query Match 84.2%; Score 32; DB 1; Length 139;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYWI 5
Db 52 WYWI 56

RESULT 6
US-08-436-717-35
Sequence 35, Application US/08436717
Patent No. 581790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-35

Query Match 84.2%; Score 32; DB 2; Length 139;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYWI 5
Db 52 WYWI 56

RESULT 7
5223610-5
Patent No. 5223610
APPLICANT: Burton, Frank H.; Sutcliffe, Gregor
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
HORMONE PROMOTER
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,852
FILING DATE: 18-MAY-1990
SEQ ID NO: 5
LENGTH: 266
5223610-5

Query Match 84.2%; Score 32; DB 6; Length 266;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYWIA 6
Db 52 WYWIA 6

Db 15 WLWMLA 20

RESULT 8

5244657-5
; Patent No. 5244657
; APPLICANT: KLIEN, MICHEL A.; BOUX, HEATHER A.; COCKLE,
; STEPHEN A.; LOOSMORE, SHEENA M.; ZEALY, GAVIN R.
; TITLE OF INVENTION: GENETIC DETOXIFICATION OF PERTUSSIS
; TOXIN
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/589,423
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 275,376
; FILING DATE: 23-NOV-1988
; SEQ ID NO: 5
; LENGTH: 269

Query Match

Best Local Similarity 84.2%; Score 32; DB 6; Length 269;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLWMLA 6
| | | | |
Db 15 WLWMLA 20

RESULT 9

5433945-5
; Patent No. 5433945
; APPLICANT: KLEIN, MICHEL H.; BOUX, HEATHER A.; COCKLE,
; STEPHEN A.; LOOSMORE, SHEENA M.; ZEALY, GAVIN R.
; TITLE OF INVENTION: IMMUNOPROTECTIVE GENETICALLY-DETOXIFIED
; MUTANTS OF PERTUSSIS TOXIN
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/979,798
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 589,423
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: 275,376
; FILING DATE: 23-NOV-1988
; SEQ ID NO: 5
; LENGTH: 269

Query Match

Best Local Similarity 84.2%; Score 32; DB 6; Length 269;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLWMLA 6
| | | | |
Db 15 WLWMLA 20

RESULT 10

US-09-122-126B-2
; Sequence 2, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-122-126B-2

Query Match

Best Local Similarity 84.2%; Score 32; DB 4; Length 837;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWML 5
| | | | |
Db 33 WLWML 37

RESULT 11

US-08-469-260A-534
; Sequence 534, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MIERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUTIK
; APPLICANT: ISA K. MUSHAMMAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 534:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-534

Query Match

Best Local Similarity 81.6%; Score 31; DB 4; Length 50;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWMLA 6
| | | | |
Db 3 WVVWVS 8

RESULT 12

US-09-316-080-5
; Sequence 5, Application US/09316080
; Patent No. 6180366
; GENERAL INFORMATION:
; APPLICANT: John C. Royer
; APPLICANT: Lynne M. Christlanson
; APPLICANT: Gregory A. Gambetta
; APPLICANT: Howard Brody
; APPLICANT: Suzanne M. Otani
; TITLE OF INVENTION: Methods For Producing Heterologous
; TITLE OF INVENTION: Polypeptides In Trichothecene-Deficient Filamentous Fungal
; FILE REFERENCE: 5563.200-US
; CURRENT APPLICATION NUMBER: US/09/316,080
; EARLIER FILING DATE: 1999-05-20
; EARLIER FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 377
; ORGANISM: Fusarium
US-09-316-080-5

Query Match

Best Local Similarity 81.6%; Score 31; DB 4; Length 377;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWI 5
1:11:

DB 220 WWWW 224

RESULT 13

US-09-316-080-2
; Sequence 2, Application US/09316080
; Patent No. 6180366
; GENERAL INFORMATION:
; APPLICANT: John C. Royer
; APPLICANT: Lynne M. Christlanson
; APPLICANT: Gregory A. Gambetta
; APPLICANT: Howard Brody
; APPLICANT: Suzanne M. Otani
; APPLICANT: Wendy T. Yoder
; TITLE OF INVENTION: Methods For Producing Heterologous
; TITLE OF INVENTION: Polypeptides In Trichothecene-Deficient Filamentous Fungal
; FILE REFERENCE: 5563.200-US
; CURRENT APPLICATION NUMBER: US/09/316,080
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: 09/082,217
; EARLIER FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Fusarium
US-09-316-080-2

Query Match

Best Local Similarity 81.6%; Score 31; DB 4; Length 380;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWI 5
1:11:

DB 220 WWWW 224

RESULT 14

US-08-952-365-2
; Sequence 2, Application US/08952365
; Patent No. 6274311
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A Method and Nucleotide Sequence for
; Patent No. 6274311
; TITLE OF INVENTION: Transforming Microorganisms
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERSKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3T2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/952,365
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 6580-63
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-952-365-2

Query Match

Best Local Similarity 81.6%; Score 31; DB 4; Length 438;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWI 5
1:11:

DB 133 WWWW 137

RESULT 15

US-08-663-566A-19
; Sequence 19, Application US/08663566A
; Patent No. 5853733
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/663,566A
 FILING DATE: June 13, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)278-0400
 TELEFAX: (212)391-0526
 TELEX: 422523
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 705 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-663-566A-19

Query Match 81.6% Score 31; DB 2; Length 705;
 Best Local Similarity 66.7%; Pred No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WLWIA 6
 1 1 1 1
 Db 640 WYVWLA 645

Search completed: January 3, 2003, 15:34:32
 Job time : 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:32:11 : Search time 4.77273 Seconds
(without alignments)
23.825 Million cell updates/sec

Title: US-09-543-188a-27

Perfect score: 38
Sequence: 1 WLWVIA 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PC1_NEM_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PC1US_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	97.4	230	9	US-09-738-626-3571
2	34	89.5	49	10	US-09-995-494-75
3	34	89.5	420	10	US-09-815-242-11260
4	33	86.8	296	10	US-09-741-669-378
5	33	86.8	735	10	US-09-815-242-12089
6	32	84.2	75	8	US-08-424-550B-478
7	32	84.2	110	10	US-09-867-550-298
8	32	84.2	560	10	US-09-815-242-11746
9	32	84.2	837	12	US-10-052-586-352
10	31	81.6	50	8	US-08-424-550B-534
11	31	81.6	73	10	US-09-864-761-37732
12	31	81.6	86	10	US-09-864-761-48030
13	31	81.6	96	10	US-09-864-761-33793
14	31	81.6	126	10	US-09-864-761-48848
15	31	81.6	401	10	US-09-871-874-11
16	31	81.6	438	10	US-08-894-993-2
17	31	81.6	441	10	US-09-871-874-21
18	31	81.6	441	10	US-09-895-686-1
19	31	81.6	445	9	US-09-992-598-177

20	31	81.6	445	9	US-09-989-293A-177	Sequence 177, App
21	31	81.6	445	9	US-10-063-547-32	Sequence 32, Appl
22	31	81.6	445	9	US-09-989-735-177	Sequence 177, App
23	31	81.6	445	9	US-09-990-444-177	Sequence 177, App
24	31	81.6	445	9	US-09-989-730-177	Sequence 177, App
25	31	81.6	445	9	US-09-990-436-177	Sequence 177, App
26	31	81.6	445	9	US-09-991-181-177	Sequence 177, App
27	31	81.6	445	9	US-09-993-687-177	Sequence 177, App
28	31	81.6	445	10	US-09-989-722-177	Sequence 177, App
29	31	81.6	445	10	US-09-989-723-177	Sequence 177, App
30	31	81.6	445	10	US-09-989-279-177	Sequence 177, App
31	31	81.6	445	10	US-09-989-727-177	Sequence 177, App
32	31	81.6	445	10	US-09-989-727-177	Sequence 177, App
33	31	81.6	445	10	US-09-989-731-177	Sequence 177, App
34	31	81.6	445	10	US-09-989-732-177	Sequence 177, App
35	31	81.6	445	10	US-09-991-073-177	Sequence 177, App
36	31	81.6	445	10	US-09-990-442-177	Sequence 177, App
37	31	81.6	445	10	US-09-991-163-177	Sequence 177, App
38	31	81.6	445	10	US-09-993-604-177	Sequence 177, App
39	31	81.6	445	10	US-09-990-456-177	Sequence 177, App
40	31	81.6	445	12	US-10-006-867-32	Sequence 32, Appl
41	31	81.6	445	12	US-10-052-586-148	Sequence 148, App
42	31	81.6	446	9	US-09-738-626-6356	Sequence 6356, Ap
43	31	81.6	446	10	US-09-871-874-10	Sequence 10, Appl
44	31	81.6	446	10	US-09-951-780-2	Sequence 2, Appl
45	31	81.6	451	10	US-09-871-874-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-738-626-3571
; Sequence 3571, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3571
; LENGTH: 230
; TYPE: PR
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3571

Query Match 97.4%; Score 37; DB 9; Length 230;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
||:||||
DB 170 WLWVIA 175

```
RESULT 2
US-09-995-494-75
; Sequence 75, Application us/09995494
; Patent No. US20020127578A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; APPLICANT: Chen, Sei-Yu
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0293
; CURRENT APPLICATION NUMBER: US/09/995,494
; CURRENT FILING DATE: 2001-11-27
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-995-494-75

Query Match
Best Local Similarity 89.5%; Score 34; DB 10; Length 49;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVIA 6
|:|:|
Db 8 WVWVVA 13

RESULT 3
US-09-815-242-11260
; Sequence 11260, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11260
; LENGTH: 420
; TYPE: PRT
```

```
; ORGANISM: Haemophilus influenzae
US-09-815-242-11260

Query Match
Best Local Similarity 89.5%; Score 34; DB 10; Length 420;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVI 5
|:|:|
Db 10 WLWVI 14

RESULT 4
US-09-741-669-378
; Sequence 378, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 378
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-378

Query Match
Best Local Similarity 86.8%; Score 33; DB 10; Length 296;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVI 5
|:|:|
Db 44 WLWVI 48

RESULT 5
US-09-815-242-12089
; Sequence 12089, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
```

PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12089
LENGTH: 735
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12089

Query Match 86.8%; Score 33; DB 10; Length 735;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWVI 5
Db 469 WLWVI 473

RESULT 6

US-08-424-550B-478
Sequence 478, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMJ J. PILOT-MATIAS
APPLICANT: GEORGE J. DANSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 478:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-478

Query Match 84.2%; Score 32; DB 8; Length 75;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLWVIA 6
Db 2 WLWVIA 7

RESULT 7

US-09-867-550-298
Sequence 298, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells a
FILE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 298
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (37)
OTHER INFORMATION: wherein Xaa may be any one of Ser or Pro or Thr or Ala
US-09-867-550-298

Query Match 84.2%; Score 32; DB 10; Length 110;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLWVIA 6
Db 84 WLWVIA 89

RESULT 8

US-09-815-242-11746
Sequence 11746, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11746
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-815-242-11746

Query Match 84.28; Score 32; DB 10; Length 560;
 Best Local Similarity 83.38; Pired. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYVIA 6
 ||||
 Db 146 WLSMIA 151

RESULT 9

; -10-052-586-352
 ; Sequence 352, Application US/10052586
 ; Patent No. US20020127584A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C1

; CURRENT APPLICATION NUMBER: US/10/052,586
 ; CURRENT FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063564
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063734
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063870
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066120
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/066466
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066772

; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/069335
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069425
 ; PRIOR FILING DATE: 1997-12-12
 ; PRIOR APPLICATION NUMBER: 60/069870
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/068017
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077649
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/078886
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078939
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079664
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079786
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/080107
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080194
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080327
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080333
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082704
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083495
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083496
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083499
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083559
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084640
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086486
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087098
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087208
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088740
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088825
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089090
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653

PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089908

Query Match 84.2%; Score 32; DB 12; Length 837;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWMI 5
Db 33 WLWVL 37

RESULT 10

US-08-424-550B-534
Sequence 534, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATTIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MIERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIK
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSER: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ. ID NO: 534:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-534

Query Match 81.6%; Score 31; DB 8; Length 50;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLWMI 6
Db 3 WVVWVS 8

RESULT 11
US-09-864-761-37732
Sequence 37732, Application US/09864761

QY 1 WLVWIA 6
1:111
DB 76 WLVWIA 81

RESULT 13
US-09-864-761-33793
; Sequence 33793, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33793
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009307.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.97

OTHER INFORMATION: SWISSPROT HIT: Q23445, EVALU 3.80e+00
; OTHER INFORMATION: EST HUMAN HIT: A0119728.1, EVALU 1.00e-38
; OTHER INFORMATION: EST_HUMAN HIT: BE069876.1, EVALU 8.00e-03
US-09-864-761-33793

Query Match 81.6%; Score 31; DB 10; Length 96;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WLVWIA 6
11111
DB 80 WLVWIA 85

RESULT 14
US-09-864-761-48848
; Sequence 48848, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmca-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48848
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010368.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4

OTHER INFORMATION: SWISSPROT HIT: P27958, EVALUE 7.50e-01
 OTHER INFORMATION: EST_HUMAN HIT: A1472010.1, EVALUE 2.00e-57
 US-09-864-761-48848

Query Match 81.6%; Score 31; DB 10; Length 126;
 Best Local Similarity 80.0%; Pred. No. 90;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMI 5
 1:111
 Db 110 WVWMI 114

RESULT 15
 US-09-871-874-11
 Sequence 11, Application US/09871874
 Patent No. US20020081655A1
 GENERAL INFORMATION:

APPLICANT: SAVITZKY, Kinneret
 APPLICANT: TOPORIK, Amir
 APPLICANT: MINTZ, Liat
 TITLE OF INVENTION: Splice Variant of mGluR
 FILE REFERENCE: 2786-0176P
 CURRENT APPLICATION NUMBER: US/09/871, 874
 CURRENT FILING DATE: 2001-09-04
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 11
 LENGTH: 401
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-871-874-11

Query Match 81.6%; Score 31; DB 10; Length 401;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLWMI 5
 1:111
 Db 256 WVWMI 260

Search completed: January 3, 2003, 15:52:07
 Job time : 4.77273 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:00 ; Search time 9.95455 seconds
(without alignments)
57.944 Million cell updates/sec

Title: US-09-543-188A-23

Perfect score: 36

Sequence: 1 IFFWLK 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	91.7	101	2	B87530
2	32	88.9	73	2	D81622
3	32	88.9	73	2	S59082
4	32	88.9	374	2	T32207
5	32	88.9	423	2	E90569
6	32	88.9	544	2	T51162
7	32	88.9	660	2	AE3226
8	32	88.9	988	2	H71338
9	31	86.1	86	2	AD0850
10	31	86.1	162	2	D69381
11	31	86.1	247	2	T33469
12	31	86.1	258	2	AC2542
13	31	86.1	262	2	S75891
14	31	86.1	267	2	A72238
15	31	86.1	287	2	T02338
16	31	86.1	388	2	S57526
17	31	86.1	398	2	H70142
18	31	86.1	400	2	H97550
19	31	86.1	400	2	AH2770
20	31	86.1	449	2	C86496
21	31	86.1	449	2	D72127
22	31	86.1	449	2	A81544
23	31	86.1	474	2	S41117
24	31	86.1	495	1	S25942
25	31	86.1	497	1	S53834
26	31	86.1	500	2	F88921
27	31	86.1	507	1	A30828
28	31	86.1	513	2	B70478
29	31	86.1	532	2	G82872

30	31	86.1	564	2	T20191	hypothetical prote
31	31	86.1	597	2	T27497	hypothetical prote
32	31	86.1	639	1	S45776	uracil transport p
33	31	86.1	669	2	I54205	galactosylceramid
34	31	86.1	738	2	S10659	membrane protein
35	31	86.1	826	1	A31822	villin - chicken
36	31	86.1	951	1	SYECVT	valine-tRNA ligase
37	31	86.1	951	2	C91283	valine-tRNA synth
38	31	86.1	951	2	E86124	valine-tRNA synth
39	31	86.1	951	2	AC1061	valine-tRNA ligase
40	31	86.1	955	2	F84972	valine-tRNA ligase
41	31	86.1	963	2	T12087	H+-exporting ATPas
42	31	86.1	965	2	AE0418	valine-tRNA ligase
43	31	86.1	966	2	T52413	H+-exporting ATPas
44	31	86.1	1101	2	T33153	hypothetical prote
45	31	86.1	1113	2	S48495	probable membrane

ALIGNMENTS

RESULT 1
B87530
hypothetical protein CC2267 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: B87530
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:1125647
A:Accession: B87530
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <STO>
A:Cross-references: GB:AE005673; NID:g13423780; PIDN:AAK24238.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2267

Query Match 91.7%; Score 33; DB 2; Length 101;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 IFFWLK 6
DB 6 VFFWLK 11
RESULT 2
D81622
hypothetical protein CP0010 [imported] - Chlamydia pneumoniae (strain AR39)
C:Species: Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: D81622
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gili, S.R.; Heidelberg, J.F.; White, O.; Hicke , C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: D81622
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-35 <RFA>
A:Cross-references: GB:AE002165; GB:AE002161; NID:g7188948; PIDN:AAF37906.1; PTD:g718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0010
Query Match 88.9%; Score 32; DB 2; Length 35;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
11111
DB 12 IFFWIK 17

RESULT 3

SS9082
hypothetical protein 73 - red alga (*Chondrus crispus*) mitochondrion
C:Species: mitochondrion *Chondrus crispus* (carrageen)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jul-2000
C:Accession: SS9082
R:Leblanc, C.; Boyen, C.; Richard, O.; Bonnard, G.; Grienenberger, J.M.; Kloareg, B.
J. Mol. Biol. 250, 484-495, 1995
A>Title: Complete sequence of the mitochondrial DNA of the rhodophyte *Chondrus crispus*
A:Reference number: SS9078; MUID:95341681; PMID:7616569
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-73 <LEB>
A:Cross-references: EMBL:Z47547; NID:q1019057; PIDN:CA87598.1; PID:q1334478
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 88.9%; Score 32; DB 2; Length 73;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 IFFWIK 6
11111
DB 38 IFFWIK 43

RESULT 4

T32207
hypothetical protein T03D3.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32207
R:Murray, J.; Wohldmann, P.; Bauer, C.; Blewald, T.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of *C. elegans* cosmid T03D3.
A:Reference number: Z21136
A:Accession: T32207
A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-374 <MUR>
A:Cross-references: EMBL:AF022980; PIDN:AAB69912.1; GSPDB:GN00023; CESP:T03D3.5
A:Experimental source: strain Bristol N2; clone T03D3
C:Genetics:
A:Gene: CESP:T03D3.5
A:Map position: 5
A:Introns: 17/3; 28/3; 43/2; 93/3; 155/3; 209/2; 244/2

Query Match 88.9%; Score 32; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FFWIK 6
11111
DB 36 FFWIK 40

RESULT 5

E90569
conserved hypothetical protein MYPu_4610 [imported] - *Mycoplasma pulmonis* (strain UAB CT
C:Species: *Mycoplasma pulmonis*.
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: E90569

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer,
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma p*
A:Reference number: A95512; MUID:21267165; PMID:11353084

A:Accession: E90569
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-423 <KUR>
A:Cross-references: GB:AL445566; PID:q14089875; PIDN:CA013634.1; GSPDB:GN00153
A:Experimental source: strain UAB CT1P
C:Genetics:
A:Gene: MYPu_4610
A:Genetic code: SGC3

Query Match 88.9%; Score 32; DB 2; Length 423;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
11111
DB 390 IFFWIK 395

RESULT 6

T51162
aminoglycoside acetyltransferase regulator [imported] - *Providencia stuartii*
C:Species: *Providencia stuartii*
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000
C:Accession: T51162
R:MacInga, D.R.; Cook, G.M.; Poole, R.K.; Rather, P.N.
J. Bacteriol. 180, 128-135, 1998
A>Title: Identification and characterization of *aarf*, a locus required for production
arti.

A:Reference number: Z25318; MUID:98083065; PMID:9422602
A:Accession: T51162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-544 <MAC>
A:Cross-references: EMBL:AF002165; PIDN:AAB96577.1
A:Experimental source: strain PR50
C:Genetics:
A:Gene: *aarf*
C:Superfamily: Synchocystis ABC transporter slr1919

Query Match 88.9%; Score 32; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FFWIK 6
11111
DB 41 FFWIK 45

RESULT 7

AE3226
conserved hypothetical protein Atus541 [imported] - *Agrobacterium tumefaciens* (strain
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AE3226
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guentherer, D.; Kutyavin, T.; Levy, R.; Li, M.; MCI
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AE3226
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-660 <KUR>
A:Cross-references: GB:AE008687; PIDN:AAL46227.1; PID:q17744003; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)

C:Genetics:
A:Gene: Atu5541
A:Genome: plasmid

Query Match 88.9%; Score 32; DB 2; Length 660;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
DB 358 IFFWIK 363

RESULT 8

conserved hypothetical protein TP0325 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: H71338

A:Author: C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; PMID:98332770; PMID:9665876
A:Accession: H71338

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-968 <COLD>
A:Cross-references: GB:AE001212; GB:AE00520; NID:g3322597; PIDN:AAC65312.1; PID:g332260
A:Experimental source: strain Nichols
C:Genetics:

A:Gene: TP0325
C:Superfamily: syphilis spirochete conserved hypothetical protein TP0325

Query Match 88.9%; Score 32; DB 2; Length 988;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFWIK 6
DB 747 FFWIK 751

RESULT 9

AD0850
doubtful CDS found within S. typhi pathogenicity island [imported] - Salmonella enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AD0850

A:Author: R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AD0850
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05987.1; PID:g16503958; GSPDB:GN00176
C:Genetics:

A:Gene: STY3003

Query Match 86.1%; Score 31; DB 2; Length 86;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
DB 53 LFFWIK 58

RESULT 10

D69381
hypothetical protein AF1052 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69381

A:Author: R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; PMID:98049343; PMID:9389475
A:Accession: D69381
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <KLE>

A:Cross-references: GB:AE001030; GB:AE000782; NID:g2689353; PIDN:AB90193.1; PID:g264
Query Match 86.1%; Score 31; DB 2; Length 162;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
DB 68 VFFWIK 73

RESULT 11

T33469
hypothetical protein F43B10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C:Accession: T33469

A:Author: R.Fulton, R.; Hawkins, J.; Rohlfing, T.
A:Title: The sequence of C. elegans cosmid F43B10.
A:Reference number: Z21351
A:Accession: T33469
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-247 <FUL>

A:Cross-references: EMBL:AF096500; PIDN:AAC67400.1; GSPDB:GN00028; CESP:F43B10.1
A:Experimental source: strain Bristol N2; clone F43B10
C:Genetics:
A:Gene: CESP:F43B10.1
A:Map position: X
A:Introns: 88/2; 103/3; 128/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F43B10.1

Query Match 86.1%; Score 31; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 5
DB 85 IFFWIK 89

RESULT 12

AG2542
hypothetical protein all7626 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC712
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AG2542

A:Author: R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iri
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2542
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: GB:AP003602; PIDN:BAW77269.1; PID:gl7134711; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all7626
A:Genome: plasmid

Query Match
Best Local Similarity 86.1%; Score 31; DB 2; Length 258;
100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWI 5
|||||
DB 20 IFFWI 24

ULT 13
891

hypothetical protein slr1174 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.

A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75891

R:Kaneko, T.; Sato, S.; Kohani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A:title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
5.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S75891

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-262 <KAN>

A:Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BA18350.1; PID:d101908
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match

Best Local Similarity 86.1%; Score 31; DB 2; Length 262;
100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWI 5
|||||
DB 26 IFFWI 30

ULT 14
A72238

hemolysin - *Thermotoga maritima* (strain MSB8)

C:Species: *Thermotoga maritima*

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: A72238

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999

A:title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: A72238

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-267 <ARN>

A:Cross-references: GB:AE001802; GB:AE000512; NID:g4982133; PIDN:AAD36643.1; PID:g498214

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1576

C:Superfamily: hemolysin homolog yqxc

Query Match
Best Local Similarity 86.1%; Score 31; DB 2; Length 267;
80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 FFWK 6
|||||
DB 237 FFWK 241

RESULT 15
T05338

hypothetical protein F1C12.211 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C:Accession: T05338

R:Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De Clerck, R.;
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15408

A:Accession: T05338

A:Molecule type: DNA

A:Residues: 1-287 <BEV>

A:Cross-references: EMBL:AL022224

A:Experimental source: cultivar Columbia; BAC clone F1C12

C:Genetics:

A:Map position: 4

A:Introns: 37/2; 116/2; 243/3; 269/3

A:Note: F1C12.211

Query Match
Best Local Similarity 86.1%; Score 31; DB 2; Length 287;
80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FFWK 6
|||||
DB 53 FFWK 57

Search completed: January 3, 2003, 15:33:19
Job time : 10.9545 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:22:10 ; Search time 5.18182 Seconds
(without alignments)
48.025 Million call updates/sec

Title: US-09-543-188a-23
Perfect score: 36
Sequence: 1 IFFWIK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112392

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	88.9	544	UBIB_PROST	O07443 providencia
2	31	86.1	162	YA52_ARCFU	Q29210 archaeoglob
3	31	86.1	367	NUIC_MESVI	Q9m011 mesosigma
4	31	86.1	473	NORB_PSEST	P98008 pseudomonas
5	31	86.1	495	NUAM_MARPO	P26848 marchantia
6	31	86.1	497	NUAM_MARPO	Q37375 acanthamoeb
7	31	86.1	507	CPT7_RAT	P11715 rattus norv
8	31	86.1	639	FU11_YEAST	P38196 saccharomyc
9	31	86.1	669	GALC_CANFA	P54804 canis famli
10	31	86.1	669	GALC_HUMAN	P54803 homo sapien
11	31	86.1	669	GALC_HUMAN	O02791 macaca mula
12	31	86.1	684	ATY3_HUMAN	Q9h7f0 homo sapien
13	31	86.1	717	TRD1_ECOLI	P09130 escherichia
14	31	86.1	738	TRD2_ECOLI	P22708 escherichia
15	31	86.1	826	VILI_CHICK	P02640 gallus gall
16	31	86.1	951	SVY_ECOLI	P07118 escherichia
17	31	86.1	955	SVY_BUCAT	P57447 buchnera ap
18	31	86.1	1113	WGA2_YEAST	P40578 saccharomyc
19	31	86.1	1256	FLU1_DROME	Q24020 drosophila
20	30	83.3	110	RT10_PEA	P51428 pisum sativ
21	30	83.3	142	RADC_COXBU	O85403 coxiella bu
22	30	83.3	349	YB64_SYNY3	P73771 synechocyst
23	30	83.3	367	NUIC_TOBAC	P06254 nicotiana t
24	30	83.3	368	NUIC_MARPO	P06255 marchantia
25	30	83.3	381	CYB_CARCA	P34665 cartharodon
26	30	83.3	381	CYB_ISUPA	P34671 isurus pauc
27	30	83.3	411	LAG1_YEAST	P38703 saccharomyc
28	30	83.3	470	MM12_HUMAN	P39900 homo sapien
29	30	83.3	537	AREH_SCHPO	O10269 schizosacch
30	30	83.3	642	YAZA_SCHPO	Q09701 schizosacch
31	30	83.3	668	GALC_MOUSE	P54818 mus musculu
32	30	83.3	826	VILI_HUMAN	P09327 homo sapien
33	30	83.3	826	VILI_MOUSE	Q62468 mus musculu

34	30	83.3	865	1	SVY_THEMA	Q9x2d7 thermotoga
35	30	83.3	875	1	SVY_BORBU	O51680 borrelia bu
36	30	83.3	880	1	SVY_BACBD	O9x898 bacillus ha
37	30	83.3	880	1	SVY_BACST	P11931 bacillus st
38	30	83.3	880	1	SVY_BACSU	Q05873 bacillus su
39	30	83.3	910	1	SVY_SYNY3	O55522 synechocyst
40	30	83.3	945	1	SVY_NEIMA	O91x22 neisseria m
41	30	83.3	945	1	SVY_NEIMB	O91x17 neisseria m
42	30	83.3	953	1	SVY_VIRCH	O9x873 vibrio chol
43	30	83.3	954	1	SVY_HAEIN	P43834 haemophilus
44	30	83.3	956	1	SVY_TREPA	O83998 treponema p
45	30	83.3	960	1	PMA4_ARATH	O9su58 arabidopsis

ALIGNMENTS

```

RESULT 1
UBIB_PROST          STANDARD:      PRT:      544 AA.
ID  UBIB_PROST
AC  O07443;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Probable ubiquitinone biosynthesis protein ubib (aminoglycoside
DE  acetyltransferase regulator).
GN  UBIB OR AARF.
OS  Providencia stuartii.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX  Providencia.
ON  NCBI_TaxID=588;
OR  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PR50;
RX  MEDLINE=98083065; PubMed=9422602;
RA  Macinga D.R., Cook G.M., Poole R.K., Rather P.N.;
RT  Identification and characterization of aarf, a locus required for
RT  production of ubiquinone in Providencia stuartii and Escherichia coli
RT  and for expression of 2'-N-acetyltransferase in P. stuartii.;
RL  J. Bacteriol. 180:128-135(1998).
RN  [2]
RP  CHARACTERIZATION.
RC  STRAIN=PR50;
RX  MEDLINE=20416225; PubMed=10960098;
RA  Poon W.W., Davis D.E., Ha H.T., Jonassen T., Rather P.N., Clarke C.F.;
RT  Identification of Escherichia coli ubib, a gene required for the
RT  first monooxygenase step in ubiquinone biosynthesis.;
RL  J. Bacteriol. 182:5139-5146(2000).
CC  -1- FUNCTION: REQUIRED, PROBABLY INDIRECTLY, FOR THE HYDROXYLATION OF
CC  2-OCTAPRENYLPHENOL TO 2-OCTAPRENYL-6-HYDROXY-PHENOL, THE FOURTH
CC  STEP IN UBIQUINONE BIOSYNTHESIS. REQUIRED FOR THE EXPRESSION OF
CC  2'-N-ACETYLTTRANSFERASE.
CC  -1- SIMILARITY: BELONGS TO THE ABC1 FAMILY. UBIB SUBFAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AF002165; AAB96577.1; -.
DR  InterPro: IPR004147; ABC1.
DR  Pfam: PF03109; ABC1; 1.
KW  Ubiquinone biosynthesis.
SQ  SEQUENCE 544 AA; 62598 MW; E789A4E8185B4F96 CRC64;
Query Match          88.9%; Score 32; DB 1; Length 544;
Best local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  2 FFWIK 6

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Db 41 FFWIK 45

RESULT 2

YAS2_ARCFU STANDARD; PRT; 162 AA.
ID YAS2_ARCFU
AC 029210;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF1052 precursor.
GN AF1052.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RA MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriakides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Arlanch P., Kalne B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.V., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).

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CC EMBL: AE01030; AAB90193.1; -
CC DR TIGR: AF1052; -
CC KW Hypothetical protein; Signal; Complete proteome.
CC SIGNAL 1 34
CC CHAIN 35 162
CC SEQUENCE 162 AA; 18043 MW; A6547DC1139B72B3 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 162;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
Db 68 YFEWVK 73

RESULT 3

NOIC_MESVI STANDARD; PRT; 367 AA.
AC 09MU11;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-plastoquinone oxidoreductase chain 1, chloroplast (EC 1.6.5.3).
GN NDHA.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.

OX NCBI_TaxID=41882;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-296;
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
RT branch of green plant evolution.";
RL Nature 403:649-653(2000).
CC -1- CATALYTIC ACTIVITY: NADH + plastoquinone -> NAD(+) + plastoquinol.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.

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CC EMBL: AF166114; AAF43887.1; -
CC DR InterPro: IPR001694; Resp_NADH_dhl.
CC DR Pfam: PF00146; NADHdn; 1.
CC DR PROSITE: PS00667; COMPLEX1_ND1_1; FALSE_NEG.
CC DR PROSITE: PS00668; COMPLEX1_ND1_2; 1.
CC KW Oxidoreductase; NAD; Plastoquinone; Chloroplast; Transmembrane.
SQ SEQUENCE 367 AA; 40369 MW; 158CF9E4A58EB98 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 5
Db 132 IFFWIK 136

RESULT 4

NORB_PSEST STANDARD; PRT; 473 AA.
AC P98008;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nitric oxide reductase subunit B (EC 1.7.99.7) (Nitric oxide reductase
DE cytochrome b subunit) (NOR large subunit).
GN NORB.

OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC STRAIN=ATCC 14405 / Zobell;
RX MEDLINE=94139726; PubMed=7508388;
RA Zumft W.G., Braun C., Cuyper H.;
RT "Nitric oxide reductase from Pseudomonas stutzeri. Primary structure
RT and gene organization of a novel bacterial cytochrome bc complex.";
RL Eur. J. Biochem. 219:481-490(1994).

RN [2]
RP EPR SPECTROSCOPY.
RC STRAIN=ATCC 14405 / Zobell;
RX MEDLINE=89255095; PubMed=2542222;
RA Heiss B., Frunzke K., Zumft W.G.;
RT "Formation of the N-N bond from nitric oxide by a membrane-bound
RT cytochrome bc complex of nitrate-respiring (denitrifying) Pseudomonas
RT stutzeri.";
RL J. Bacteriol. 171:3288-3297(1989).

RN [3]
RP EPR SPECTROSCOPY.
RC STRAIN=ATCC 14405 / Zobell;
RX MEDLINE=98191362; PubMed=9521721;
RA Cheesman M.R., Zumft W.G., Thomson A.J.;

RT "The MCD and EPR of the heme centers of nitric oxide reductase
 RT from *Pseudomonas stutzeri*: evidence that the enzyme is
 RT structurally related to the heme-copper oxidases.";
 RL Biochemistry 37:3994-4000(1998).
 CC -1- FUNCTION: COMPONENT OF THE ANAEROBIC RESPIRATORY CHAIN THAT
 CC TRANSFORMS NITRATE TO DINITROGEN (DENITRIFICATION). NORB IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME COMPLEX. SHOWS PROTON PUMP
 CC ACTIVITY ACROSS THE MEMBRANE IN DENITRIFYING BACTERIAL CELLS. THE
 CC MONONITROGEN REDUCTION IS PROBABLY COUPLED TO ELECTRON TRANSPORT
 CC PHOSPHORYLATION
 CC -1- CATALYTIC ACTIVITY: Nitrous oxide + acceptor + H(2)O = 2 nitric
 CC oxide + reduced acceptor.
 CC -1- SUBUNIT: HETERODIMER OF CYTOCHROMES B (LARGE SUBUNIT) AND C (SMALL
 CC SUBUNIT).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- INDUCTION: BY NITRIC OXIDE (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z28384; CAAB2229.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PROSITE: PS00077; COX1.1.
 KW Oxidoreductase; Heme; Iron; Transmembrane; Respiratory chain.
 FT INIT_MET 0 0
 FT METAL 59 59 IRON (LOW-SPIN HEME) (PROBABLE).
 FT METAL 206 206 IRON B (PROBABLE).
 FT METAL 257 257 IRON B (PROBABLE).
 FT METAL 258 258 IRON B (PROBABLE).
 FT METAL 346 346 IRON (HIGH-SPIN HEME) (PROBABLE).
 FT METAL 348 348 IRON (LOW-SPIN HEME) (PROBABLE).
 FT TRANSMEM 18 38 POTENTIAL.
 FT TRANSMEM 60 80 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 144 164 POTENTIAL.
 FT TRANSMEM 168 188 POTENTIAL.
 FT TRANSMEM 206 226 POTENTIAL.
 FT TRANSMEM 242 262 POTENTIAL.
 FT TRANSMEM 269 289 POTENTIAL.
 FT TRANSMEM 307 327 POTENTIAL.
 FT TRANSMEM 347 367 POTENTIAL.
 FT TRANSMEM 389 409 POTENTIAL.
 FT TRANSMEM 432 452 POTENTIAL.
 SQ SEQUENCE 473 AA; 53006 MW; 39E999DC1DD7F757 CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 473;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 IFFWIK 6
 Db 434 IFFWIK 439
 RESULT 5
 NU4M_MARPO STANDARD: PRT: 495 AA.
 AC P26848;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1994 (Rel. 38, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
 GN NDA OR NAD4.
 OS Marchantia polymorpha (Liverwort).
 OG Mitochondrion.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;

OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiaceae;
 OC Marchantiaceae; Marchantia.
 OX NCBI_TaxID=3197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92114051; PubMed=1731062;
 RA Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N.,
 RA Akashi K., Kaneage T., Ogura Y., Kohchi T., Ohyama K.;
 RT "Gene organization deduced from the complete sequence of liverwort
 RT Marchantia polymorpha mitochondrial DNA. A primitive form of plant
 RT mitochondrial genome.";
 RL J. Mol. Biol. 223:1-7(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93247547; PubMed=8483448;
 RA Nozato N., Oda K., Yamato K., Ohta E., Takemura M., Akashi K.,
 RA Fukuzawa H., Ohyama K.;
 RT "Clonally transcribed expression of mitochondrial genes for subunits of
 RT NADH dehydrogenase, nad5, nad4, nad2, in Marchantia polymorpha.";
 RL Mol. Gen. Genet. 237:343-350(1993).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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 CC -----
 DR EMBL: M68929; AAC09398.1; -
 DR PIR: S25942; S25942.
 DR InterPro: IPR003918; NADHUB_OXRED4.
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; Oxidored_q1.1.
 DR PRINTS: PR01437; NUOXDRDTASE4.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 495 AA; 56311 MW; 0F75894D6CAAAED4 CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 495;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 IFFWIK 6
 Db 53 IFFWIK 58
 RESULT 6
 NU4M_ACACA STANDARD: PRT: 497 AA.
 AC Q37373;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
 GN NDA OR NAD4.
 OS Acanthamoeba castellanii (Amoeba).
 OG Mitochondrion.
 OC Eukaryota; Acanthamoebidae; Acanthamoeba.
 OX NCBI_TaxID=5755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 30010 / NEFF;
 RX MEDLINE=95147275; PubMed=7844823;
 RA Burger G., Plante I., Loneragan K.M., Gray M.W.;
 RT "The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba
 RT castellanii: complete sequence, gene content and genome
 RT organization.";
 RL J. Mol. Biol. 245:522-537(1995).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -----
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CC -----
 CC EMBL: U12386; AAD11826.1; -
 CC InterPro: IPR003918; NADhub_oxred4.
 CC InterPro: IPR001750; Oxidored.q1.
 CC Pfam: PF00361; oxidored.q1.1.
 CC PRINTS: PR01437; NUOXDRDTASE4.
 CC Oxidoreductase; NAD: Ubiquinol.
 CC SEQUENCE 497 AA; 57768 MW; 9C0B637E65C0F3B5 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 497;
 Best Local Similarity 100.0%; Pred. NO. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IFFWI 5
 53 IFFWI 57

RESULT 7
 CPT7_RAT STANDARD: PRT; 507 AA.

AC P11715;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome P450 17 (EC 1.14.99.9) (CYPXVII) (P450-C17) (Steroid
 DE 17-alpha-hydroxylase/17,20 lyase).
 GN CYP17
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 OX 11
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=89295447; PubMed=2786990;
 RA Revold H.R., Lorence W.C., McCarthy J.L., Trant J.M., Kagimoto M.,
 RA Waterman M.R., Mason J.I.;
 RT "Rat P450(C17 alpha) from testis: characterization of a full-length
 RT cDNA encoding a unique steroid hydroxylase capable of catalyzing both
 RT delta 4- and delta 5-steroid-17,20-lyase reactions.";
 RL Mol. Endocrinol. 3:968-975(1989).
 RL [2]
 P1 SEQUENCE FROM N.A.
 P1 TISSUE=Testis;
 RX MEDLINE=89076306; PubMed=3264499;
 RA Namiki M., Kitamura M., Buczek E., Dufau M.L.;
 RT "Rat testis P-450(17)alpha cDNA: the deduced amino acid sequence,
 RT expression and secondary structural configuration.";
 RL Biochem. Biophys. Res. Commun. 157:705-712(1988).
 RL [3]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Sprague-Dawley;
 RX MEDLINE=95217329; PubMed=7702752;
 RA Glvens C.R., Zhang P., Balr S.R., Mellon S.H.;
 RT "Transcriptional regulation of rat cytochrome P450c17 expression in
 RT mouse Leydig MA-10 and adrenal Y-1 cells: identification of a single
 RT protein that mediates both basal and CAMP-induced activities.";
 RL DNA Cell Biol. 13:1087-1098(1994).
 RL [4]
 RP SEQUENCE OF 271-507 FROM N.A.
 RP MEDLINE=88280759; PubMed=3260774;
 RA Nishihara M., Winters C.A., Buzko E., Waterman M.R., Dufau M.L.;
 RT "Hormonal regulation of rat Leydig cell cytochrome P-45017 alpha
 RT levels and characterization of a partial length rat P-45017 alpha
 RT cDNA.";
 RL Biochem. Biophys. Res. Commun. 154:151-158(1988).
 RL [5]

RP SEQUENCE OF 273-507 FROM N.A.
 RX MEDLINE=90046678; PubMed=2554289;
 RA Mellon S.H., Valses C.;
 RT "cAMP regulates P450sc gene expression by a
 RT cyclonximide-insensitive mechanism in cultured mouse Leydig MA-10
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7775-7779(1989).
 CC -1- FUNCTION: CONVERSION OF PREGNENOLONE AND PROGESTERONE TO THEIR
 CC 17-ALPHA-HYDROXYLATED PRODUCTS AND SUBSEQUENTLY TO
 CC DEHYDROEPIANDROSTERONE (DHEA) AND ANDROSTERONE. CATALYZES
 CC BOTH THE 17-ALPHA-HYDROXYLATION AND THE 17,20-LYASE REACTION.
 CC INVOLVED IN SEXUAL DEVELOPMENT DURING FETAL LIFE AND AT PUBERTY.
 CC -1- CATALYTIC ACTIVITY: A steroid + AH(2) + O(2) = a 17-alpha-
 CC hydroxysteroid + A + H(2)O.
 CC -1- ENZYME REGULATION: REGULATED PREDOMINANTLY BY INTRACELLULAR CAMP
 CC LEVELS.
 CC -1- PATHWAY: KEY ENZYME IN STEROIDGENIC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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CC -----
 CC EMBL: X14086; CAA32248.1; -
 CC EMBL: X69816; CAA49470.1; -
 CC EMBL: M31681; AAA41777.1; -
 CC EMBL: M22204; AAA41783.1; -
 CC EMBL: M21208; AAA41050.1; -
 CC EMBL: M27282; AAA41779.1; -
 CC PIR: A27659; A27659.
 CC PIR: A30828; A30828.
 CC PIR: S16719; S16719.
 CC HSSP: P00179; 1DT6.
 CC InterPro: IPR001128; Cytochrome_p450.
 CC Pfam: PF00067; P450; 1.
 CC PRINTS: PR00385; P450.
 CC PROSITE: PS00086; CYTOCHROME_P450; 1.
 CC Electron transport; Oxidoreductase; Monooxygenase; Membrane;
 KW Heme; Steroidogenesis.
 FT BINDING 441 441 HEME (BY SIMILARITY).
 FT CONFLICT 505 506 VS -> LT (IN REF. 4).
 SQ SEQUENCE 507 AA; 57250 MW; A535600F7E6A3999 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. NO. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFWIK 6
 Db 15 PFWIK 19

RESULT 8
 PUI1_YEAST STANDARD: PRT; 639 AA.

ID P38196;
 AC P38196;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Uridine permease.
 GN PUI1 OR YBL042C OR YBL0406.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN RP SEQUENCE FROM N.A.
 RP STRAIN=S288C;
 RX MEDLINE=95176707; PubMed=7871888;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta, and SKIN fibroblast;
RA MEDLINE=9412808; PubMed=8297359;
RA Sakai N., Inui K., Fujii N., Fukushima H., Nishimoto J.,
RA Yanagihara I., Isegawa Y., Iwamatsu A., Okada S.;
RT "Krabbe disease: isolation and characterization of a full-length cDNA
RT for human galactocerebrosidase.";
RL Biochem. Biophys. Res. Commun. 198;485-491(1994).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-59 AND 436-454.
RC TISSUE=Brain, and Testis;
RA MEDLINE=94108435; PubMed=8281145;
RA Chen Y.O., Rafi M.A., de Gail G., Wenger D.A.;
RT "Cloning and expression of cDNA encoding human galactocerebrosidase,
RT the enzyme deficient in globoid cell leukodystrophy.";
RN Hum. Mol. Genet. 2;1841-1845(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=95324938; PubMed=7601472;
RA Luzi P., Rafi M.A., Wenger D.A.;
RT "Structure and organization of the human galactocerebrosidase (GALC)
RT gene.";
RN Genomics 26;407-409(1995).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=98094242; PubMed=9434153;
RA Sakai N., Fukushima H., Inui K., Fu L., Nishigaki T., Yanagihara I.,
RA Tatsumi N., Ozono K., Okada S.;
RT "Human galactocerebrosidase gene: promoter analysis of the 5'-flanking
RT region and structural organization.";
RN Biochim. Biophys. Acta 1395;62-67(1998).
RN [5]
RP SEQUENCE OF 27-45 AND 436-454, AND CHARACTERIZATION.
RC TISSUE=Urine;
RA MEDLINE=94002192; PubMed=8399327;
RA Chen Y.O., Wenger D.A.;
RT "Galactocerebrosidase from human urine: purification and partial
RT characterization.";
RN Biochim. Biophys. Acta 1170;53-61(1993).
RN [6]
RP REVIEW ON GLD MUTATIONS.
RA MEDLINE=97478285; PubMed=9338580;
RA Wenger D.A., Rafi M.A., Luzi P.;
RT "Molecular genetics of Krabbe disease (globoid cell leukodystrophy):
RT diagnostic and clinical implications.";
RN Hum. Mutat. 10;268-279(1997).
RN [7]
RP VARIANTS GLD ALA-302 AND GLY-550.
RA MEDLINE=96121583; PubMed=8595408;
RA Tatsumi N., Inui K., Sakai N., Fukushima H., Nishimoto J.,
RA Yanagihara I., Nishigaki T., Tsukamoto H., Fu L., Tanike M.,
RA Okada S.;
RT "Molecular defects in Krabbe disease.";
RN Hum. Mol. Genet. 4;1865-1868(1995).
RN [8]
RP VARIANTS GLD ASN-528 AND SER-583.
RA MEDLINE=96198195; PubMed=8786069;
RA Rafi M.A., Luzi P., Zlotogora J., Wenger D.A.;
RT "Two different mutations are responsible for Krabbe disease in the
RT Druse and Moslem Arab populations in Israel.";
RN Hum. Genet. 97;304-308(1996).
RN [9]
RP FUNCTION: HYDROLYSES THE GALACTOSE ESTER BONDS OF
CC GALACTOSYLCERAMIDE, GALACTOSYLSPHINGOSINE, LACTOSYLCERAMIDE, AND
CC MONOGLACTOSYLGLYCERIDE. ENZYME WITH VERY LOW ACTIVITY
CC RESPONSIBLE FOR THE LYSOSOMAL CATABOLISM OF GALACTOSYLCERAMIDE, A
CC MAJOR LIPID IN MYELIN, KIDNEY AND EPITHELIAL CELLS OF SMALL
CC INTESTINE AND COLON. HAS AN OPTIMAL PH BETWEEN 4.0 AND 4.4.
CC ACTIVITY IS LOST WHEN HEATED AT 52 DEGREES CELSIUS FOR FIVE
CC MINUTES.

CC -I- CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine + H(2)O = D-
CC galactose + N-acylsphingosine.
CC -I- SUBCELLULAR LOCATION: Lysosomal.
CC -I- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE LONG FORM.
CC -I- TISSUE SPECIFICITY: HIGHEST LEVEL OF ACTIVITY IN TESTES COMPARED
CC TO BRAIN, KIDNEY, PLACENTA AND LIVER. CAN ALSO BE FOUND IN URINE.
CC -I- DISEASE: DEFECTS IN GALC ARE THE CAUSE OF GLOBOID CELL
CC LEUKODYSTROPHY (GLD) (OR KRABBE DISEASE). THIS AUTOSOMAL RECESSIVE
CC DISORDER DEFICIENCY RESULTS IN THE INSUFFICIENT CATABOLISM OF
CC SEVERAL GALACTOLIPIDS THAT ARE IMPORTANT IN THE PRODUCTION OF
CC NORMAL MYELIN. CLINICALLY THE MOST FREQUENT FORM IS THE INFANTILE
CC FORM. MOST PATIENTS (90%) PRESENT BEFORE SIX MONTHS OF AGE WITH
CC IRRITABILITY, SPASTICITY, ARREST OF MOTOR AND MENTAL DEVELOPMENT,
CC AND BOUTS OF TEMPERATURE ELEVATION WITHOUT INFECTION. THIS IS
CC FOLLOWED BY MYOCLONIC JERKS OF ARMS AND LEGS, OPHTHOMOUS,
CC HYPERONIC FITS, AND MENTAL REGRESSION, WHICH PROGRESSES TO A
CC SEVERE DECELERATE CONDITION WITH NO VOLUNTARY MOVEMENTS AND DEATH
CC FROM RESPIRATORY INFECTIONS OR CEREBRAL HYPERTENSIA BEFORE 2
CC YEARS OF AGE. HOWEVER, A SIGNIFICANT NUMBER OF CASES WITH LATER
CC ONSET, PRESENTING WITH UNEXPLAINED BLINDNESS, WEAKNESS AND/OR
CC PROGRESSIVE MOTOR, AND SENSORY NEUROPATHY THAT CAN PROGRESS TO
CC SEVERE MENTAL INCAPACITY AND DEATH, HAVE BEEN IDENTIFIED.
CC -I- SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D25283; BAA04971.1; -;
DR EMBL: D25284; BAA04972.1; -;
DR EMBL: L23116; AAA16643.1; -;
DR EMBL: L38559; AAA80975.1; JOINED.
DR EMBL: L38544; AAA80975.1; JOINED.
DR EMBL: L38545; AAA80975.1; JOINED.
DR EMBL: L38547; AAA80975.1; JOINED.
DR EMBL: L38547; AAA80975.1; JOINED.
DR EMBL: L38548; AAA80975.1; JOINED.
DR EMBL: L38549; AAA80975.1; JOINED.
DR EMBL: L38550; AAA80975.1; JOINED.
DR EMBL: L38551; AAA80975.1; JOINED.
DR EMBL: L38552; AAA80975.1; JOINED.
DR EMBL: L38553; AAA80975.1; JOINED.
DR EMBL: L38555; AAA80975.1; JOINED.
DR EMBL: L38556; AAA80975.1; JOINED.
DR EMBL: L38557; AAA80975.1; JOINED.
DR EMBL: L38558; AAA80975.1; JOINED.
DR EMBL: D84181; BAA24902.1; JOINED.
DR EMBL: D84232; BAA24902.1; JOINED.
DR EMBL: D84233; BAA24902.1; JOINED.
DR EMBL: D84234; BAA24902.1; JOINED.
DR EMBL: D84266; BAA24902.1; JOINED.
DR EMBL: D84267; BAA24902.1; JOINED.
DR EMBL: D84268; BAA24902.1; JOINED.
DR EMBL: D84269; BAA24902.1; JOINED.
DR EMBL: D84363; BAA24902.1; JOINED.
DR EMBL: D84364; BAA24902.1; JOINED.
DR EMBL: D84365; BAA24902.1; JOINED.
DR EMBL: D84366; BAA24902.1; JOINED.
DR EMBL: D84367; BAA24902.1; JOINED.
DR EMBL: D84368; BAA24902.1; JOINED.
DR EMBL: D84369; BAA24902.1; JOINED.
DR EMBL: D84393; BAA24902.1; JOINED.
DR GENE: HGNC:4115; GALC.
DR MIM: 606890; -;
DR MIM: 245200; -;
DR INTERPRO: IPR001286; GH_59.
DR Pfam: PF02057; Glyco_hydro_59; 1.
DR PRINTS: PR00850; GLHYDRASE59.

KW Hydrolase; Glycosidase; Glycoprotein; Signal; Alternative splicing;
KW Disease mutation; Polymorphism.
FT SIGNAL 1 26
FT CARBOHYD 127 669 GALACTOCEREBROSIDASE.
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARBPLIC 372 391 SHKHSKTRPPIPRVSO -> VIFCCYVINSLLYWK
FT VARBPLIC 392 669 NKT (IN SHORT ISOFORM).
FT VARBPLIC 95 95 MISSING (IN SHORT ISOFORM).
FT VARBPLIC 95 95 G -> D (IN GLD).
FT VARBPLIC 95 95 /FTID-VAR_003380.
FT VARBPLIC 95 95 G -> S (IN GLD).
FT VARBPLIC 96 96 /FTID-VAR_003381.
FT VARBPLIC 96 96 T -> A (IN GLD; ADULT).
FT VARBPLIC 101 101 /FTID-VAR_003382.
FT VARBPLIC 101 101 M -> L (IN GLD; ADULT).
FT VARBPLIC 171 171 /FTID-VAR_003383.
FT VARBPLIC 171 171 D -> V (IN GLD).
FT VARBPLIC 178 178 /FTID-VAR_003384.
FT VARBPLIC 178 178 G -> A (IN GLD).
FT VARBPLIC 232 232 /FTID-VAR_003385.
FT VARBPLIC 232 232 D -> N.
FT VARBPLIC 234 234 /FTID-VAR_003386.
FT VARBPLIC 234 234 I -> T (IN GLD; LATE INFANTILE).
FT VARBPLIC 247 247 /FTID-VAR_003387.
FT VARBPLIC 247 247 A -> T (IN GLD).
FT VARBPLIC 268 268 /FTID-VAR_003388.
FT VARBPLIC 268 268 G -> S (IN GLD).
FT VARBPLIC 270 270 /FTID-VAR_003389.
FT VARBPLIC 270 270 G -> D (IN GLD).
FT VARBPLIC 279 279 /FTID-VAR_003390.
FT VARBPLIC 279 279 N -> T (IN GLD).
FT VARBPLIC 287 287 /FTID-VAR_003391.
FT VARBPLIC 287 287 S -> F (IN GLD).
FT VARBPLIC 302 302 /FTID-VAR_003392.
FT VARBPLIC 302 302 P -> A (IN GLD).
FT VARBPLIC 380 380 /FTID-VAR_003393.
FT VARBPLIC 380 380 R -> W (IN GLD; BILATERAL CHERRY RED SPOTS).
FT /FTID-VAR_003394.
Query Match 86.1%; Score 31; DB 1; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Luzi P., Rafi M.A., Victoria T., Baskin G.B., Wenger D.A.;
RT "Characterization of the rhesus monkey galactocerebrosidase (GALC)
RT cDNA and gene and identification of the mutation causing globoid cell
RT leukodystrophy (Krabbe disease) in this primate.";
RL Genomics 42:319-324(1997).
CC -1- FUNCTION: HYDROLASES THE GALACTOSE ESTER BONDS OF
CC GALACTOSYLCERAMIDE, GALACTOSYLSPHINGOSINE, LACTOSYLCERAMIDE, AND
CC MONOGALACTOSYLDIGLYCERIDE. ENZYME WITH VERY LOW ACTIVITY.
CC RESPONSIBLE FOR THE LYSOSOMAL CATABOLISM OF GALACTOSYLCERAMIDE, A
CC MAJOR LIPID IN MYELIN, KIDNEY AND EPITHELIAL CELLS OF SMALL
CC INTESTINE AND COLON (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine + H(2)O = D-
CC galactose + N-acylsphingosine.
CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -1- DISEASE: DEFECTS IN GALC ARE THE CAUSE OF GLOBOID CELL
CC LEUKODYSTROPHY (GLD) (OR KRABBE DISEASE). THIS DEFICIENCY RESULTS
CC IN THE INSUFFICIENT CATABOLISM OF SEVERAL GALACTOLIPIDS THAT ARE
CC IMPORTANT IN THE PRODUCTION OF NORMAL MYELIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; U87477; AAB58575.1; JOINED.
DR EMBL; U87462; AAB58575.1; JOINED.
DR EMBL; U87463; AAB58575.1; JOINED.
DR EMBL; U87464; AAB58575.1; JOINED.
DR EMBL; U87465; AAB58575.1; JOINED.
DR EMBL; U87466; AAB58575.1; JOINED.
DR EMBL; U87467; AAB58575.1; JOINED.
DR EMBL; U87468; AAB58575.1; JOINED.
DR EMBL; U87469; AAB58575.1; JOINED.
DR EMBL; U87470; AAB58575.1; JOINED.
DR EMBL; U87471; AAB58575.1; JOINED.
DR EMBL; U87472; AAB58575.1; JOINED.
DR EMBL; U87473; AAB58575.1; JOINED.
DR EMBL; U87474; AAB58575.1; JOINED.
DR EMBL; U87475; AAB58575.1; JOINED.
DR EMBL; U87476; AAB58575.1; JOINED.
DR EMBL; U87628; AAB58576.1; JOINED.
DR InterPro: IPR001286; GH_59.
DR Pfam: PF02057; Glyco_hydro_59; 1.
DR PRINTS: PR00850; GLHYDRLASE59.
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 668 GALACTOCEREBROSIDASE.
FT CARBOHYD 127 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 669 AA: 75206 MW; F09169DECB66C07 CRC64;
Query Match 86.1%; Score 31; DB 1; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable cation-transporting ATPase 3 (EC 3.6.3.-) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Coronary artery;
 RA Kawabata A., Hiki J. T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEO human cDNA sequencing project."
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 ATPASES). SUBFAMILY V.

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 DR EMBL: AK024639; BAB1942.1; ALT_INIT.
 DR InterPro: IPR001757; ATPase_E1-E2.
 DR InterPro: IPR001454; Hlgase/hydrase.
 DR Pfam: PF00702; Hydrase: 1.
 DR PRINTS: PR00119; CATATPASE.
 DR PROSITE: PS00154; ATPase_E1_E2: 1.
 KM Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.
 FT NON-TER 1 1
 FT TRANSMEM 10 29 POTENTIAL.
 FT TRANSMEM 44 64 POTENTIAL.
 FT TRANSMEM 537 556 POTENTIAL.
 FT TRANSMEM 568 585 POTENTIAL.
 FT TRANSMEM 602 622 POTENTIAL.
 FT TRANSMEM 659 671 POTENTIAL.
 FT MOD_RES 97 97 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 482 482 MAGNESIUM (BY SIMILARITY).
 FT METAL 486 486 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 684 AA: 76081 MW: D655E494DCEAE1E7 CRC64;

 DT Query Match 86.1%; Score 31; DB 1; Length 684;
 DT Best Local Similarity 80.0%; Pred. No. 1; Seq-ID: 02;
 DT Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 2 FFWIK 6
 DB 624 FFWIK 628

 RESULT 13
 TRD1_ECOLI STANDARD; PRT: 717 AA.
 ID TRD1_ECOLI
 AC P09130;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Trad protein.
 GN TRAD.
 OS Escherichia coli.
 OG Plasmid F.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NC NCBL_TaxID=562;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=K12;
 RX MEDLINE=90034191; PubMed=2680768;
 RA Jalajakumari M.B., Manning P.A.;
 RT "Nucleotide sequence of the trad region in the Escherichia coli F sex
 RT factor."
 RL gene 81:195-202(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359430; PubMed=7915817;
 RA Frost L.S., Ippen-Ihler K., Skurray R.A.;
 RT "Analysis of the sequence and gene products of the transfer region of
 RT the F sex factor."
 RL Microbiol. Rev. 58:162-210(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / CR63;
 RA Shimizu H., Saitoh Y., Suda Y., Uehara K., Sempel G., Mizobuchi K.;
 RT "Complete nucleotide sequence of the F plasmid: its implications for
 RT organization and diversification of plasmid genomes."
 RL submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 8-34 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=88118903; PubMed=3323526;
 RA Jalajakumari M.B., Guidolin A., Buhj H.J., Manning P.A.;
 RT "Surface exclusion genes tras and trat of the F sex factor of
 RT Escherichia coli K-12. Determination of the nucleotide sequence and
 RT promoter and terminator activities."
 RL J. Mol. Biol. 198:1-11(1987).
 RN [5]
 RP SEQUENCE OF 462-717 FROM N.A.
 RX MEDLINE=90299847; PubMed=2163400;
 RA Bradshaw H.D. Jr., Traxler B.A., Minkley E.G. Jr., Nester E.W.,
 RA Gordon M.P.;
 RT "Nucleotide sequence of the trait (hellicase I) gene from the sex
 RT factor F."
 RL J. Bacteriol. 172:4127-4131(1990).
 RN [6]
 RP SEQUENCE OF 1-102 AND 665-717 FROM N.A.
 RX MEDLINE=90317835; PubMed=2164585;
 RA Yoshioke Y., Fujita Y., Ohtsubo E.;
 RT "Nucleotide sequence of the promoter-distal region of the tra operon
 RT of plasmid R100, including trait (DNA helicase I) and trad genes."
 RL J. Mol. Biol. 214:39-53(1990).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=92316963; PubMed=1618779;
 RA Panicker M.M., Minkley E.G. Jr.;
 RT "Purification and properties of the F sex factor Trad protein, an
 RT inner membrane conjugal transfer protein."
 RL J. Biol. Chem. 267:12761-12766(1992).
 RN [8]
 RP TOPOLOGY.
 RX MEDLINE=94429860; PubMed=10498725;
 RA Lee M.H., Kosuk N., Bailey J., Traxler B., Mancil C.;
 RT "Analysis of F factor Trad membrane topology by use of gene fusions
 RT and trypsin-sensitive insertions."
 RL J. Bacteriol. 181:6108-6113(1999).
 CC -1- FUNCTION: TRAD IS A CELL ENVELOPE PROTEIN. THE FUNCTION OF TRAD
 CC IS UNKNOWN BUT IT IS ESSENTIAL FOR DNA TRANSFER. IT MAY FORM OR
 CC MAY BE PART OF A NON-SPECIFIC PORE FOR DNA EXPORT, OR IT MAY
 CC DIRECTLY ENERGIZES DNA TRANSFER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: TO THE TRAD OF PLASMID INCFIT R100.

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DR EMBL: M29254; AAA83928.1; -
DR EMBL: U01159; AAC4181.1; -
DR EMBL: AP001918; BAA97972.1; -
DR EMBL: X06915; CAA30013.1; ALT_SEQ.
DR EMBL: M54796; AAA98083.1; -
DR EMBL: X57431; CAA40678.1; -
DR EMBL: X57428; CAA40674.1; -
DR PIR: J50293; BVECAD.
DR PIR: S01758; S01758.
DR EcoGene: EG40117; trad.
DR InterPro: IPR003688; TRAG.
DR Pfam: PF02534; TRAG; 1.
KW Plasmid; Inner membrane; Conjugation; Transmembrane; ATP-binding;
KW Complete proteome.
FT DOMAIN 1 27 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 28 47 PROBABLE.
FT DOMAIN 48 104 PERIPLASMIC (PROBABLE).
FT TRANSMEM 105 130 PROBABLE.
FT DOMAIN 131 717 CYTOPLASMIC (PROBABLE).
FT NP_BIND 192 199 ATP (POTENTIAL).
FT CONFLICT 19 47 IMMEDIATELY ADJACENT TO YPHVOPDR
OYHALPYEFLDTRSGFMD (IN REF. 1 AND 6).
IMFSQIANIMLCLEF -> YPHVOPDRYHALPY
(IN REF. 4).
FT CONFLICT 19 34 QTF -> TDV (IN REF. 1 AND 6).
FT CONFLICT 52 54 QTF -> TDV (IN REF. 1 AND 6).
FT CONFLICT 58 62 CIYWW -> LFTV (IN REF. 1 AND 6).
FT CONFLICT 190 190 R -> L (IN REF. 3).
FT CONFLICT 269 270 RD -> PM (IN REF. 3).
FT CONFLICT 321 325 VIHRQ -> RNSPA (IN REF. 3).
SQ SEQUENCE 717 AA; 81683 MW; F4B564EDD90EB914 CRC64;

Query Match
Best Local Similarity 86.1%; Score 31; DB 1; Length 717;
Matches 5; Conservative 100.0%; Pred. No. 1.6e+02;
Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
DB 35 IFFWI 39

RESULT 14
TRD2_ECOLI
ID TRD2_ECOLI STANDARD; PRT; 738 AA.
AC P22708;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
RT Trad protein.
RA Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317835; PubMed=2164585;
RA Yoshioke Y., Fujita Y., Ohtsubo E.;
RT "Nucleotide sequence of the promoter-distal region of the tra operon
of plasmid R100, including traI (DNA helicase I) and trad genes.";
J. Mol. Biol. 214:39-53(1990).
-1- FUNCTION: TRAD IS A CELL ENVELOPE PROTEIN. THE FUNCTION OF TRAD
IS UNKNOWN BUT IT IS ESSENTIAL FOR DNA TRANSFER. IT MAY FORM OR
MAY BE PART OF A NON-SPECIFIC PORE FOR DNA EXPORT, OR IT MAY
DIRECTLY ENERGIZES DNA TRANSPORT.
-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-1- SIMILARITY: TO THE TRAD OF PLASMID F.
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DR EMBL: X55815; CAA39336.1; -
DR PIR: S10659; S10659.
DR InterPro: IPR003688; TRAG.
DR Pfam: PF02534; TRAG; 1.
KW Plasmid; Inner membrane; Conjugation; Transmembrane; ATP-binding;
KW Repeat.
FT TRANSMEM 28 44 POTENTIAL.
FT TRANSMEM 113 129 POTENTIAL.
FT TRANSMEM 396 413 POTENTIAL.
FT NP_BIND 192 199 ATP (POTENTIAL).
FT DOMAIN 617 646 10 X 3 AA TANDEM REPEATS OF Q-Q-P.
SQ SEQUENCE 738 AA; 83900 MW; 84CB1F48245E766F CRC64;

Query Match
Best Local Similarity 86.1%; Score 31; DB 1; Length 738;
Matches 5; Conservative 100.0%; Pred. No. 1.6e+02;
Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
DB 35 IFFWI 39

RESULT 15
VILLI_CHICK
ID VILLI_CHICK STANDARD; PRT; 826 AA.
AC P02640;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Villin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88276884; PubMed=2839826;
RA Bazari W.L., Matsudaira P., Waller M., Smeal T., Jakes R., Ahmed Y.;
RT "Villin sequence and peptide map identify six homologous domains.";
Proc. Natl. Acad. Sci. U.S.A. 85:4986-4990(1988).
RN [2]
RP SEQUENCE OF 751-826.
RX MEDLINE=81264203; PubMed=6790532;
RA Glenney J.R., Jr., Geisler N., Kaulfus P., Weber K.;
RT "Demonstration of at least two different actin-binding sites in
villin, a calcium-regulated modulator of F-actin organization.";
J. Biol. Chem. 256:8156-8161(1981).
RN [3]
RP CALCIUM-BINDING SITES.
RX MEDLINE=83082892; PubMed=6848508;
RA Hesterberg L.K., Weber K.;
RT "Demonstration of three distinct calcium-binding sites in villin, a
modulator of actin assembly.";
J. Biol. Chem. 258:365-369(1983).
RN [4]
RP STRUCTURE BY NMR OF 1-127.
RX MEDLINE=94191534; PubMed=8142900;
RA Markus M.A., Nakayama T., Matsudaira P., Wagner G.;
RT "Solution structure of villin 14T, a domain conserved among actin-
severing proteins.";
Protein Sci. 3:70-81(1994).
RN [5]
RP STRUCTURE BY NMR OF 1-127.
RX MEDLINE=97337440; PubMed=9194180;
RA Markus M.A., Matsudaira P., Wagner G.;
RT "Refined structure of villin 14T and a detailed comparison with other
actin-severing domains.";
Protein Sci. 6:1197-1209(1997).
RN [6]

```


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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:24:35 ; Search time 20.3183 Seconds
(without alignments)
60.846 Million cell updates/sec

Title: US-09-543-188a-23

Perfect score: 36
Sequence: 1 IFFWK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL_21:*
1: sp._archaea:*
2: sp._bacteria:*
3: sp._fungi:*
4: sp._human:*
5: sp._invertebrate:*
6: sp._mammal:*
7: sp._mhc:*
8: sp._organelle:*
9: sp._phage:*
10: sp._plant:*
11: sp._rodent:*
12: sp._virus:*
13: sp._vertebrate:*
14: sp._unclassified:*
15: sp._viral:*
16: sp._bacteriap:*
17: sp._archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	97.2	707	5	095XL6
2	34	94.4	158	2	093ST6
3	34	94.4	409	2	0926D5
4	33	91.7	62	12	091FW6
5	33	91.7	101	16	09A628
6	33	91.7	580	2	0926G8
7	32	88.9	73	8	036329
8	32	88.9	112	2	08VNI1
9	32	88.9	113	13	09PW03
10	32	88.9	120	16	09CMX2
11	32	88.9	174	2	0916G8
12	32	88.9	174	2	08VM06
13	32	88.9	423	16	098Q05
14	32	88.9	666	10	09FDV6
15	32	88.9	671	16	08UDJ6
16	32	88.9	819	12	091EJ5

17	32	88.9	849	12	093125	093125 human calic
18	32	88.9	988	16	083345	083345 treponema p
19	32	88.9	2280	12	08U280	08U280 human calic
20	31	86.1	32	9	09MCP6	09MCP6 bacterioph
21	31	86.1	74	8	09MTD6	09MTD6 toxoplasma
22	31	86.1	86	16	08ZMI0	08ZMI0 salmonella
23	31	86.1	86	16	08Z496	08Z496 salmonella
24	31	86.1	174	2	P97065	P97065 salmonella
25	31	86.1	174	2	P97066	P97066 salmonella
26	31	86.1	174	2	P97067	P97067 salmonella
27	31	86.1	174	2	P97068	P97068 salmonella
28	31	86.1	174	2	P97231	P97231 salmonella
29	31	86.1	180	2	P71251	P71251 escherichia
30	31	86.1	180	2	P71252	P71252 escherichia
31	31	86.1	180	2	P71253	P71253 escherichia
32	31	86.1	180	2	P71254	P71254 escherichia
33	31	86.1	180	2	P71255	P71255 escherichia
34	31	86.1	180	2	P71256	P71256 escherichia
35	31	86.1	180	2	P71257	P71257 escherichia
36	31	86.1	180	2	P71258	P71258 escherichia
37	31	86.1	180	2	P71259	P71259 escherichia
38	31	86.1	180	2	P71260	P71260 escherichia
39	31	86.1	180	2	P71261	P71261 escherichia
40	31	86.1	180	2	P75018	P75018 escherichia
41	31	86.1	190	2	09KTA9	09KTA9 escherichia
42	31	86.1	190	2	09KTA8	09KTA8 escherichia
43	31	86.1	225	9	064371	064371 lactobacill
44	31	86.1	258	9	09A2P8	09A2P8 bacterioph
45	31	86.1	258	16	08ZS86	08ZS86 anabaena sp

ALIGNMENTS

RESULT 1

ID 095XL6 PRELIMINARY: PRT; 707 AA.
AC 095XL6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 79.9 KDa protein.
GN Y73E7A.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Du H., Maupin R.;
RT "The sequence of C. elegans cosmid Y73E7A.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC025727; AAK6029.1; -
DR InterPro: IPR000884; TSP1.
DR PROSITE: PS50092; TSP1.1.
KW Hypothetical protein.
SQ SEQUENCE 707 AA; 79940 MW; 26B924988153DBA8 CRC64;

Query Match 97.2%; Score 35; DB 5; Length 707;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
||||:|
DB 470 IFFWIK 475

RESULT 2

ID Q93ST6 PRELIMINARY; PRT; 158 AA.
AC Q93ST6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCHF.
GN BCHF.
OS Chlorobium tepidum.
Bacteria: Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
Chlorobium.
NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20433268; PubMed=10976061;
RA Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;
RT "Molecular evidence for the early evolution of photosynthesis.";
RL Science 289:1724-1730(2000).
DR EMBL:AT005138; AAG12430.1; -;
SQ SEQUENCE 158 AA; 18396 MW; ABFEF8FCF70B7411 CRC64;

Query Match

Best Local Similarity 94.4%; Score 34; DB 2; Length 158;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
||||:|
DB 109 IFFWIK 114

RESULT 3

ID Q926D5 PRELIMINARY; PRT; 409 AA.
AC Q926D5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE OapA.
GN Haemophilus ducreyi1.
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=35000;
MEDLINE=99115572; PubMed=9916106;
RA Bauer B.A., Lumblay S.R., Hansen E.J.;
RT "Characterization of a Waaf (Rfaf) homolog expressed by Haemophilus
ducreyi.";
RL Infect. Immun. 67:899-907(1999).
DR EMBL:AF087414; AAD16054.1; -;
SQ SEQUENCE 409 AA; 45059 MW; 2AC6861B1AC451 CRC64;

Query Match

Best Local Similarity 94.4%; Score 34; DB 2; Length 409;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
||||:|
DB 161 IFFWIK 166

RESULT 4

Q91FW6 PRELIMINARY; PRT; 62 AA.
ID Q91FW6
AC Q91FW6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 204L.
OS Chilo iridescent virus (CIV) (insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10488;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H., Darai G., Pluegel R.M.;
RT "DNA analysis of insect iridescent virus 6: evidence for circular
permutation and terminal redundancy.";
RL J. Virol. 49:609-614(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86174607; PubMed=3959991;
RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
in mice.";
RL Med. Microbiol. Immunol. 175:43-53(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321126; PubMed=2820141;
RA Schmitzler P., Soltau J.B., Fischer M., Reiser H., Scholz J.,
RA Delius H., Darai G.;
RT "Molecular cloning and physical mapping of the genome of insect
iridescent virus type 6: further evidence for circular permutation of
the viral genome.";
RL Virology 160:66-74(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073752; PubMed=3201750;
RA Fischer M., Schmitzler P., Delius H., Darai G.;
RT "Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
RL Virology 167:485-496(1988).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196996; PubMed=1549908;
RA Handermann M., Schmitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
RA Darai G.;
RT "Identification and mapping of origins of DNA replication within the
DNA sequences of the genome of insect iridescent virus type 6.";
RL Virus Genes 6:19-32(1992).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93118242; PubMed=1475907;
RA Sonntag K.C., Darai G.;
RT "Characterization of the third origin of DNA replication of the genome
of insect iridescent virus type 6.";
RL Virus Genes 6:333-342(1992).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=93260401; PubMed=8492091;
RA Stohwasser R., Raab K., Schmitzler P., Janssen W., Darai G.;
RT "Identification of the gene encoding the major capsid protein of
insect iridescent virus type 6 by polymerase chain reaction.";
RL J. Gen. Virol. 74:873-879(1993).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94167241; PubMed=8121799;
RA Schmitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
RA Delius H., Darai G.;
RT "Identification of genes encoding zinc finger proteins, non-histone
chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
in the genome of Chilo iridescent virus.";
RL Nucleic Acids Res. 22:156-166(1994).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=94353641; PubMed=8073636;

RA Sonntag K.C., Schmitzler P., Koonin E.V., Darai G.;
RT "Chilo iridescent virus encodes a putative helicase belonging to a
RT distinct family within the 'DEAD/H' superfamily: implications for the
RT evolution of large DNA viruses.";
RL Virus Genes 8:151-158(1994).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=95213160; PubMed=7698884;
RA Sonntag K.C., Schmitzler P., Janssen W., Darai G.;
RT "Identification of the primary structure and the coding capacity of
RT the genome of insect iridescent virus type 6 between the genome
RT coordinates 0.310 and 0.347 (7990 bp).";
RL Intervirology 37:287-297(1994).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292906; PubMed=8021587;
RA Schmitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
RA Koonin E.V., Darai G.;
RT "Insect iridescent virus type 6 encodes a polypeptide related to the
RT largest subunit of eukaryotic RNA polymerase II.";
RL J. Gen. Virol. 75:1557-1567(1994).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=98141693; PubMed=9482589;
RA Bahr U., Tidona C.A., Darai G.;
RT "The DNA sequence of Chilo iridescent virus between the genome
RT coordinates 0.101 and 0.391: similarities in coding strategy between
RT insect and vertebrate iridoviruses.";
RL Virus Genes 15:235-245(1997).
RN [13]
RP SEQUENCE FROM N.A.
RX MEDLINE=99125223; PubMed=9926400;
RA Muller K., Tidona C.A., Bahr U., Darai G.;
RT "Identification of a thymidylate synthase gene within the genome of
RT Chilo iridescent virus.";
RL Virus Genes 17:243-258(1998).
RN [14]
RP SEQUENCE FROM N.A.
RX MEDLINE=99383793; PubMed=10456793;
RA Muller K., Tidona C.A., Darai G.;
RT "Identification of a gene cluster within the genome of Chilo
RT iridescent virus encoding enzymes involved in viral DNA replication
RT and processing.";
RL Virus Genes 18:243-264(1999).
RN [15]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342589; PubMed=11448171;
RA Jakob N.J., Muller K., Bahr U., Darai G.;
RT "Analysis of the First Complete DNA Sequence of an Invertebrate
RT Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
RL Virology 286:182-196(2001).
RN [16]
RP SEQUENCE FROM N.A.
RA Jakob N.J., Muller K., Bahr U., Darai G.;
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF303741; AAK82066.1; -
SQ SEQUENCE 62 AA; 7876 MW; 29DF67A85F664B3E CRC64;

Query Match 91.7%; Score 33; DB 12; Length 62;
Best Local Similarity 83.3%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
DB 56 IFFWIK 61

RESULT 5
OY 09A628 PRELIMINARY; PRT; 101 AA.
AC 09A628;
DT 01-JUN-2001 (TRIMBLREL. 17, Created)
DR 01-JUN-2001 (TRIMBLREL. 17, Last sequence update)

DT 01-MAR-2002 (TRIMBLREL. 20, Last annotation update)
DE Hypothetical protein CC2267.
GN CC2267.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005897; AAK24238.1; -
DR TIGR: CC2267;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 101 AA; 11619 MW; 4B5B638942C94AF6 CRC64;

Query Match 91.7%; Score 33; DB 16; Length 101;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
DB 6 VFFWIK 11

RESULT 6
OY 0926G8 PRELIMINARY; PRT; 580 AA.
AC 0926G8;
DT 01-MAY-1999 (TRIMBLREL. 10, Created)
DT 01-MAY-1999 (TRIMBLREL. 10, Last sequence update)
DT 01-JUN-2002 (TRIMBLREL. 21, Last annotation update)
DE Polar flagellar M-ring protein FlIF.
GN FlIF.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BB22;
RX MEDLINE=20115548; PubMed=10648530;
RA Boles B.R., McCarter L.L.;
RT "Insertional inactivation of genes encoding components of the sodium-
RT type flagellar motor and switch of vibrio parahaemolyticus.";
RL J. Bacteriol. 182:1035-1045(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BB22;
RA Jaques S., Kim Y.K., McCarter L.L.;
RT "Components of the polar flagellar switch complex and assembly
RT apparatus";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF069392; AAD15920.1; -
DR InterPro: IPR000067; F1gmring_FlIF.
DR InterPro: IPR002920; YscJ_FlIF.
DR Pfam: PF01514; YscJ_FlIF; 1.
DR PRINTS: PRO1009; FLGMRINGFLIF.
DR TIGRFAMs: TIGR00206; flif; 1.
KW Flagella.
SQ SEQUENCE 580 AA; 63813 MW; 4CCE81483A047050 CRC64;

Query Match 91.7%; Score 33; DB 2; Length 580;
Best Local Similarity 66.7%; Pred. No. 3; 5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
:||||:
DB 71 LFFWIK 76

RESULT 7

Q36329 PRELIMINARY; PRT; 73 AA.
AC Q36329:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative orf73 protein.
GN PUTATIVE ORF73.
OS Chondrus crispus (Carragheen).
OC Mitochondrion.
OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartinales;
OC Chondrus.
NCBI_TaxID=2769;
[1]

SEQUENCE FROM N.A.
RC TISSUE=APICES.
RX MEDLINE=93341681; PubMed=7616569;
RA Leblanc C., Boyen C., Richard O., Bonnard G., Grienenberger J.M.,
RA Kioareg B.;
RT "Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus
crispus (Gigartinales). Gene content and genome organization.";
RL J. Mol. Biol. 250:484-495(1995).
[2]

SEQUENCE FROM N.A.
RC TISSUE=APICES.
RX MEDLINE=95395875; PubMed=7666449;
RA Leblanc C., Kioareg B., Loiseau-de Goer S., Boyen C.;
RT "DNA sequence, structure and phylogenetic relationship of the
mitochondrial small subunit rRNA from the red alga Chondrus crispus
RT (Gigartinales, Rhodophytes).";
RL J. Mol. Evol. 41:196-202(1995).
DR EMBL: 247547; CAB54039.1; -
KM Mitochondrion.
SQ SEQUENCE 73 AA; 8929 MW; 85AC46C006834292 CRC64;

Query Match 88.9%; Score 32; DB 8; Length 73;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 IFFWIK 6
:||||:
DB 38 IFFWIK 43

RESULT 8

Q8VN11 PRELIMINARY; PRT; 112 AA.
AC Q8VN11:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative DNA binding protein.
OS Lactobacillus delbrueckii (subsp. lactis).
OC Plasmid pJBL2.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Lactobacillaceae; Lactobacillus.
NCBI_TaxID=29397;
[1]

SEQUENCE FROM N.A.
RP STRAIN=JCL14;
RC Bourniquel A.A., Casey M.G., Mollet B., Pridmore R.D.;
RT "DNA sequence and functional analysis of Lactobacillus delbrueckii
RT subsp. lactis plasmids pM42 and pJBL2.";
RL Plasmid 0:0-0(0).
DR EMBL: AJ421486; CAD13351.1; -
KM Plasmid.

SQ SEQUENCE 112 AA; 13105 MW; 2EB5A6C08F8460EF CRC64;
Query Match 88.9%; Score 32; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
:||||:
DB 94 LFFWIK 99

RESULT 9

Q9PW03 PRELIMINARY; PRT; 113 AA.
AC Q9PW03:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rohu liver hypothetical protein (fragment).
GN LVHPL.
OS Labeo rohita (Indian major carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Labeo.
OX NCBI_TaxID=84645;
[1]

SEQUENCE FROM N.A.
RP TISSUE=LIVER;
RC "Partial cDNA for a hypothetical protein from Labeo rohita liver.";
RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ249232; CAB54039.1; -
KM Hypothetical protein.
FT NON_TER 1 113
SQ SEQUENCE 113 AA; 13469 MW; 6E36D649DA8FFB08 CRC64;

Query Match 88.9%; Score 32; DB 13; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 IFFWIK 6
:||||:
DB 6 IFFWIK 10

RESULT 10

Q9CMX2 PRELIMINARY; PRT; 120 AA.
AC Q9CMX2:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical protein PM0679.
GN PM0679.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
[1]

SEQUENCE FROM N.A.
RP STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL: AE006104; AAK02763.1; -
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 120 AA; 14167 MW; 46308C480002FF64 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFWIK 6
 DB 112 FFWIK 116

RESULT 11

Q9L6G8 PRELIMINARY; PRT; 174 AA.
 AC Q9L6G8;
 DT 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
 DE Putative transposase.
 OS Lactobacillus delbrueckii (subsp. bulgaricus).
 OG Plasmid pLb1.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Lactobacillaceae; Lactobacillus.
 OX NCBI_TaxID=1585;
 [1]

SEQUENCE FROM N.A.
 Accarte M.A., Raya R.R.;

RT "Structural analysis of pLb1, a cryptic plasmid from Lactobacillus
 delbrueckii subsp. bulgaricus.";
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF236060; AAF61726.1; -.
 KW Plasmid.

SO SEQUENCE 174 AA; 19597 MW; 8DDB65BCDCDB556 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 174;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
 DB 81 LFFWLK 86

RESULT 12

Q8VN06 PRELIMINARY; PRT; 174 AA.
 AC Q8VN06;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
 DE Hypothetical 19.6 kDa protein.
 OS Lactobacillus delbrueckii (subsp. lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Lactobacillaceae; Lactobacillus.
 OX NCBI_TaxID=29397;
 [1]

RP SEQUENCE FROM N.A.
 RA Bourinquel A.A., Casey M.G., Mollet B., Pridmore R.D.;

RT "DNA sequence and functional analysis of Lactobacillus delbrueckii
 subsp. lactis plasmids pM42 and pJBL2.";
 RL Plasmid 0:0-0(0).
 DR EMBL; AJ421627; CAD15746.1; -.
 KW Hypothetical protein; Plasmid.
 SO SEQUENCE 174 AA; 19555 MW; 278D0FB317C001D9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 174;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
 DB 81 LFFWLK 86

RESULT 13
 Q980A5 PRELIMINARY; PRT; 423 AA.

AC Q980A5;
 DT 01-OCT-2001 (TRENBLREL. 18, Created)
 DT 01-OCT-2001 (TRENBLREL. 18, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Hypothetical protein MYPU_4610.
 GN MYPU_4610.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 [1]

RP SEQUENCE FROM N.A.

RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chandaud I., Helling R., Ferris S., Barbe V., Samson D., Gailsson F.,
 Mosser I., Dybvig K., Wroblewski H., Viati A., Rocha E.P.C.,
 Blanchard A.;

RT "The complete genome sequence of the murine respiratory pathogen
 Mycoplasma pulmonis.";
 RL Nucleic Acids Res. 29:2145-2153(2001).
 DR EMBL; AL445564; CAC13634.1; -.
 DR Mypulist; MYPU_4610; -.
 DR InterPro; IPR004477; COMEC_N-term.
 DR TIGRFAMS; TIGR00360; COMEC_N-term; 1.
 KW Hypothetical protein; Complete proteome.

SO SEQUENCE 423 AA; 50819 MW; B4A027C3E9264F9E CRC64;

Query Match 88.9%; Score 32; DB 16; Length 423;
 Best Local Similarity 66.7%; Pred. No. 4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
 DB 390 LFFWLK 395

RESULT 14

Q9FDV6 PRELIMINARY; PRT; 666 AA.
 AC Q9FDV6;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Protein kinase.
 GN PK2.
 OS Fagus sylvatica (Beechnut).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fagales; Fagaceae; Fagus.
 OX NCBI_TaxID=28930;
 [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SEED;
 RA Lorenzo O., Rodriguez D., Nicolas C., Nicolas G.;

RT "Characterization and expression of two protein kinase genes and EIN-3
 like gene, which are regulated by ABA and GA3 in dormant Fagus
 sylvatica seeds.";
 RL (In) Black M., Bradford K.J., Vazquez-Ramos J. (eds.);
 RL SEED BIOLOGY-ADVANCES AND APPLICATIONS 32, pp.329-340,
 RL CAB International, Oxfordshire, UK (2000).
 [2]

RP SEQUENCE FROM N.A.

RC TISSUE=SEED;
 RA Lorenzo O.;

RL Thesis (2000).; Fisiologia Vegetal, Facultad de Biologia,
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ298993; CAC09581.1; -.
 DR InterPro; IPR001064; Crystalin.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.

DR PRODOM: PD000001: Euk_pkinase: 1.
DR SMART: SMO0220; S_TKC: 1.
DR SMART: SMO0219; TYRC: 1.
DR PROSITE: PS00225: CRYSTALLIN_BETAGAMMA: UNKNOWN_1.
DR PROSITE: PS00011: PROTEIN_KINASE_DOM: 1.
DR PROSITE: PS00108: PROTEIN_KINASE_ST: 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 666 AA; 74385 MW; DA586B1276259C97 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 666;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FFWIK 6
|||||
DB 369 FFWIK 373

RESULT 15

Q8UJD6 PRELIMINARY; PRT; 671 AA.

Q8UJD6;
01-JUN-2002 (TRENBLrel. 21, Created)
01-JUN-2002 (TRENBLrel. 21, Last sequence update)
01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical protein Atu5541.
GN Atu5541 OR AGR_PAT_807.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Plasmid AT.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet M., Grant C.,
Kutyavyn T., Levy R., Li W.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung W., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RT Science 294:2317-2323(2001).
RL [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Rautollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmel K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughly D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
RT Science 294:2323-2328(2001).
RL [2]
DR EMBL: AE008974; AAL6227.1; ALT_INIT.
DR EMBL: AE007922; AAK90918.1; -
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 671 AA; 72766 MW; 43EDB89528813482 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 671;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWIK 6
|||||
DB 369 IFFWIK 374

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 15:25:16 ; Search time 9 seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-543-188A-23

Perfect score: 36

Sequence: 1 IFFWIK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2.6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.4	3287	2	US-08-477-451-7
2	30	83.3	218	2	US-08-336-031-4
3	30	83.3	218	5	PCR-US95-06725-4
4	30	83.3	411	2	US-08-336-031-2
5	30	83.3	411	2	US-08-902-853-7
6	30	83.3	411	5	PCR-US95-06725-2
7	30	83.3	423	1	US-08-844-064-7
8	30	83.3	423	1	US-09-009-433-7
9	30	83.3	470	4	US-08-068-392-2
10	30	83.3	470	4	US-08-396-988-2
11	30	83.3	470	4	US-09-391-104-26
12	30	83.3	553	1	US-08-475-894-2
13	30	83.3	553	1	US-08-484-710-2
14	30	83.3	553	2	US-08-484-709-2
15	30	83.3	553	2	US-08-474-697-2
16	30	83.3	827	4	US-08-669-286-11
17	30	83.3	827	4	US-09-469-253-11
18	30	83.3	827	4	US-09-642-146-11
19	30	83.3	876	1	US-08-785-429-2
20	30	83.3	876	1	US-08-996-621-2
21	30	83.3	883	2	US-08-953-492-2
22	30	83.3	888	2	US-09-134-001C-3032
23	29	80.6	82	4	US-09-257-179-114
24	29	80.6	142	2	US-08-678-194-8
25	29	80.6	142	4	US-08-890-011-8
26	29	80.6	142	4	US-09-262-724-8
27	29	80.6	270	4	US-09-085-305-19

28	29	80.6	505	3	US-08-747-221B-14	Sequence 14, Appl
29	29	80.6	505	4	US-09-005-051-14	Sequence 14, Appl
30	29	80.6	530	3	US-08-747-221B-53	Sequence 53, Appl
31	29	80.6	530	4	US-09-005-051-53	Sequence 53, Appl
32	29	80.6	550	3	US-08-747-221B-19	Sequence 19, Appl
33	29	80.6	550	3	US-08-747-221B-58	Sequence 58, Appl
34	29	80.6	550	4	US-09-005-051-19	Sequence 19, Appl
35	29	80.6	550	4	US-09-005-051-58	Sequence 58, Appl
36	29	80.6	776	4	US-09-165-396-3	Sequence 3, Appl
37	29	80.6	1298	1	US-08-222-616-33	Sequence 33, Appl
38	29	80.6	1298	1	US-08-340-011-2	Sequence 2, Appl
39	29	80.6	1298	3	US-08-901-710-2	Sequence 2, Appl
40	29	80.6	1298	4	US-08-446-648-33	Sequence 33, Appl
41	29	80.6	1298	5	PCR-US95-04228-33	Sequence 33, Appl
42	29	80.6	1362	2	US-08-874-678-33	Sequence 33, Appl
43	29	80.6	1362	3	US-08-643-839-33	Sequence 33, Appl
44	29	80.6	1362	4	US-09-348-886-33	Sequence 33, Appl
45	29	80.6	1363	1	US-08-340-011-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-477-451-7
; Sequence 7, Application US/08477451
; Patent No. 592865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter Pylori CagI Region
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,451
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0335.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2708
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3287 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-451-7

Query Match 94.4%; Score 34; DB 2; Length 3287;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
|||||
Db 679 IFFWIK 684

RESULT 2

US-08-336-031-4
Sequence 4, Application US/08336031
Patent No. 5817782
GENERAL INFORMATION:
APPLICANT: Jazwinski, S. M.
TITLE OF INVENTION: LAG1: A GENE FOR INCREASING THE
NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: LONGEVITY OF EUKARYOTES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 93032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-031-4
Query Match 83.3%; Score 30; DB 2; Length 218;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 IFFWI 5
118 VFFWI 122
PCT-US95-06725-4
Sequence 4, Application PC/TUS9506725
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: LAG1: A GENE FOR INCREASING THE
NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: LONGEVITY OF EUKARYOTES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06725
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875 & 08/336,031
FILING DATE: 03-JUN-1994 & 08-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 93032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06725-4
Query Match 83.3%; Score 30; DB 5; Length 218;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 IFFWI 5
118 VFFWI 122
Db
RESULT 4
US-08-336-031-2
Sequence 2, Application US/08336031
Patent No. 5817782
GENERAL INFORMATION:
APPLICANT: Jazwinski, S. M.
TITLE OF INVENTION: LAG1: A GENE FOR INCREASING THE
NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: LONGEVITY OF EUKARYOTES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 93032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-336-031-2

Query Match 83.3%; Score 30; DB 2; Length 411;

Best Local Similarity 80.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5

DB 311 VFFWI 315

RESULT 5

US-08-902-853-7

Sequence 7, Application US/08902853

Patent No. 5945330

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purvi

APPLICANT: Lal, Preeti

TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,853

FILING DATE: Herewith

CLASSIFICATION: ?

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0345 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 411 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 541568

US-08-902-853-7

Query Match

Best Local Similarity

Matches 4; Conservative

QY 1 IFFWI 5

DB 311 VFFWI 315

RESULT 6

PCT-US95-06725-2

Sequence 2, Application PC/TUS9506725

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: LAG1: A GENE FOR INCREASING THE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06725

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/253,875 & 08/336,031

FILING DATE: 03-JUN-1994 & 08-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 93032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 411 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-06725-2

Query Match

Best Local Similarity

Matches 4; Conservative

QY 1 IFFWI 5

DB 311 VFFWI 315

US-08-844-064-7

Sequence 7, Application US/08844064

Patent No. 5747314

GENERAL INFORMATION:

APPLICANT: Lawlor, Elizabeth

TITLE OF INVENTION: No. 5747314el Compounds

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/844,064

FILING DATE: 18-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9607991.8
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31458-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-844-064-7

Query Match 83.3%; Score 30; DB 1; Length 423;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
DB 279 IFFWV 283

RESULT 8
US-09-009-433-7
Sequence 7, Application US/09009433
Patent No. 6087142
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6087142el Compounds
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,433
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,064
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607991.8
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31458-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-433-7

Query Match 83.3%; Score 30; DB 3; Length 423;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
DB 279 IFFWV 283

RESULT 9
US-08-068-392-2
Sequence 2, Application US/08068392
Patent No. 6150152
GENERAL INFORMATION:
APPLICANT: Shapiro, Steven M.
TITLE OF INVENTION: Human Macrophage Metalloproteinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,392
FILING DATE: 19930528
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: 07-24(12406)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-068-392-2

Query Match 83.3%; Score 30; DB 4; Length 470;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFWIK 6
DB 305 FFWIK 309

RESULT 10
US-08-396-988-2
Sequence 2, Application US/08396988
Patent No. 6204043
GENERAL INFORMATION:
APPLICANT: Shapiro, Steven M.
TITLE OF INVENTION: Human Macrophage Metalloproteinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,988
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,392
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: .07-24(12406)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-396-988-2

Query Match 83.3%; Score 30; DB 4; Length 470;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFWIK 6
|||:1
Db 305 FFWLK 309

RESULT 11
US-09-391-104-26
Sequence 26, Application US/09391104
Patent No. 6399371
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
FILE REFERENCE: 6073.US.PI
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-09-391-104-26

Query Match 83.3%; Score 30; DB 4; Length 470;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFWIK 6
|||:1
Db 305 FFWLK 309

RESULT 12
US-08-475-894-2
Sequence 2, Application US/08475894

Patent No. 5641748
GENERAL INFORMATION:
APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,894
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-475-894-2

Query Match 83.3%; Score 30; DB 1; Length 553;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
||||:
Db 68 IFFWV 72

RESULT 13
US-08-484-710-2
Sequence 2, Application US/08484710
Patent No. 5656438
GENERAL INFORMATION:
APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,710
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: BGP-190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-484-710-2

Query Match 83.3%; Score 30; DB 1; Length 553;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWI 5
||||:
68 IFFWV 72

RESULT 14
US-08-484-709-2
Sequence 2, Application US/08484709
Patent No. 5837844
GENERAL INFORMATION:
APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,709
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-484-709-2

Query Match 83.3%; Score 30; DB 2; Length 553;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWI 5
||||:
Db 68 IFFWV 72

RESULT 15
US-08-474-697-2

Sequence 2, Application US/08474697
Patent No. 6171800
GENERAL INFORMATION:
APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,697
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-474-697-2

Query Match 83.3%; Score 30; DB 4; Length 553;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IFFWI 5
||||:
Db 68 IFFWV 72

Search completed: January 3, 2003, 15:34:31
Job time : 10 secs

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: January 3, 2003, 15:32:11 ; Search time 4.77273 Seconds
(without alignments)
23.825 Million cell updates/sec

Title: US-09-543-188a-23
Perfect score: 36
Sequence: 1 IFFWIK 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

al number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	97.2	487	9 US-09-738-626-6481	Sequence 6481, App
2	31	86.1	53	10 US-09-864-761-40676	Sequence 40676, A
3	31	86.1	58	10 US-09-867-550-866	Sequence 866, App
4	31	86.1	79	10 US-09-205-658-325	Sequence 325, App
5	31	86.1	951	10 US-09-815-242-10465	Sequence 10465, A
6	31	86.1	951	10 US-09-815-242-13853	Sequence 13853, A
7	31	86.1	1256	10 US-09-935-291A-6	Sequence 6, Appl
8	30	83.3	137	10 US-09-867-550-832	Sequence 832, App
9	30	83.3	312	10 US-09-393-634-51	Sequence 51, Appl
10	30	83.3	445	9 US-09-982-598-177	Sequence 177, App
11	30	83.3	445	9 US-09-985-293A-177	Sequence 177, App
12	30	83.3	445	9 US-10-063-547-32	Sequence 32, Appl
13	30	83.3	445	9 US-09-989-735-177	Sequence 177, App
14	30	83.3	445	9 US-09-990-444-177	Sequence 177, App
15	30	83.3	445	9 US-09-989-730-177	Sequence 177, App
16	30	83.3	445	9 US-09-990-436-177	Sequence 177, App
17	30	83.3	445	9 US-09-991-181-177	Sequence 177, App
18	30	83.3	445	9 US-09-993-687-177	Sequence 177, App
19	30	83.3	445	10 US-09-989-722-177	Sequence 177, App

20	30	83.3	445	10 US-09-989-723-177	Sequence 177, App
21	30	83.3	445	10 US-09-989-279-177	Sequence 177, App
22	30	83.3	445	10 US-09-989-727-177	Sequence 177, App
23	30	83.3	445	10 US-09-989-731-177	Sequence 177, App
24	30	83.3	445	10 US-09-989-732-177	Sequence 177, App
25	30	83.3	445	10 US-09-991-073-177	Sequence 177, App
26	30	83.3	445	10 US-09-990-442-177	Sequence 177, App
27	30	83.3	445	10 US-09-991-163-177	Sequence 177, App
28	30	83.3	445	10 US-09-993-604-177	Sequence 177, App
29	30	83.3	445	10 US-09-990-456-177	Sequence 177, App
30	30	83.3	445	10 US-09-989-121-177	Sequence 177, App
31	30	83.3	445	12 US-10-006-867-32	Sequence 32, Appl
32	30	83.3	445	12 US-10-052-586-148	Sequence 148, Appl
33	30	83.3	470	9 US-09-920-455-219	Sequence 219, Appl
34	30	83.3	470	10 US-09-801-196-23	Sequence 23, Appl
35	30	83.3	473	10 US-09-925-301-1217	Sequence 1217, App
36	30	83.3	816	10 US-09-815-242-12636	Sequence 12636, A
37	30	83.3	876	10 US-09-815-242-13003	Sequence 13003, A
38	30	83.3	877	10 US-09-815-242-4876	Sequence 4876, App
39	30	83.3	879	10 US-09-815-242-5312	Sequence 5312, App
40	30	83.3	880	10 US-09-815-242-10675	Sequence 10675, A
41	30	83.3	883	10 US-09-815-242-13382	Sequence 13382, A
42	30	83.3	883	10 US-09-815-242-13684	Sequence 13684, A
43	30	83.3	950	10 US-09-815-242-11961	Sequence 11961, A
44	30	83.3	954	10 US-09-815-242-11238	Sequence 11238, A
45	29	80.6	34	10 US-09-864-761-49024	Sequence 49024, A

ALIGNMENTS

RESULT 1
US-09-738-626-6481
; Sequence 6481, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6481
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6481

Query Match 97.2% ; Score 35; DB 9; Length 487;
Best Local Similarity 83.3% ; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWIK 6
Db 412 VFWIK 417

```
RESULT 2
US-09-864-761-40676
: Sequence 40676, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aecmiga-X-1
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-07-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 40676
: LENGTH: 53
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC015473.3
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
: OTHER INFORMATION: SWISSPROT HIT: O02791, EVALUATE 1.00e-25
: OTHER INFORMATION: EST_HUMAN HIT: AW389879.1, EVALUATE 2.00e-24
US-09-864-761-40676

Query Match      86.1%, Score 31; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      1 IFFWI 5
      |||||
Db      38 IFFWI 42

RESULT 3
US-09-867-550-866
: Sequence 866, Application US/09867550
: Patent No. US20020082206A1
: GENERAL INFORMATION:
: APPLICANT: Leach, Martin D.
: APPLICANT: Mehraban, Fued,
: APPLICANT: Conley, Pamela
: APPLICANT: Law, Debbie
: APPLICANT: Topper, James
: TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells a
: FILE REFERENCE: 21402-013 (Cura-313)
: CURRENT APPLICATION NUMBER: US/09/867,550
: CURRENT FILING DATE: 2001-09-20
: PRIOR APPLICATION NUMBER: USSN 60/208,427
: PRIOR FILING DATE: 2000-05-30
: NUMBER OF SEQ ID NOS: 2125
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 866
: LENGTH: 58
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-867-550-866

Oy      2 FEWIK 6
      |||||
Db      42 FEWIK 46

RESULT 4
US-09-205-658-325
: Sequence 325, Application US/09205658
: Patent No. US20010029617A1
: GENERAL INFORMATION:
: APPLICANT: Ruvkun, Gary
: APPLICANT: Ogg, Scott
: TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
: TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
: FILE REFERENCE: 00786/351004
: CURRENT APPLICATION NUMBER: US/09/205,658
: CURRENT FILING DATE: 1998-12-03
: EARLIER APPLICATION NUMBER: 08/857,076
: EARLIER FILING DATE: 1997-05-15
: EARLIER APPLICATION NUMBER: 08/888,534
: EARLIER FILING DATE: 1997-07-07
: EARLIER APPLICATION NUMBER: US98/10080
: EARLIER FILING DATE: 1998-05-15
: NUMBER OF SEQ ID NOS: 328
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 325
: LENGTH: 79
: TYPE: PRT
: ORGANISM: Homo sapiens or Caenorhabditis elegans
US-09-205-658-325

Query Match      86.1%, Score 31; DB 10; Length 79;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 5
US-09-815-242-10465
; Sequence 10465, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10465
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10465

Query Match
Best Local Similarity 86.1%; Score 31; DB 10; Length 951;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
   |||||
   512 IFFWI 516

RESULT 6
US-09-815-242-13853
; Sequence 13853, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
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; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13853
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13853

Query Match
Best Local Similarity 86.1%; Score 31; DB 10; Length 951;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
   |||||
   512 IFFWI 516

RESULT 7
US-09-935-291A-6
; Sequence 6, Application US/09935291A
; Patent No. US20020107373A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: 49937, 49931, AND 49933, NOVEL HUMAN TRANSPORTER
; FILE REFERENCE: MNI-184
; CURRENT APPLICATION NUMBER: US/09/935,291A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/226,504
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/250,932
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-291A-6

Query Match
Best Local Similarity 86.1%; Score 31; DB 10; Length 1256;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFWK 6
   |||||
   1025 FFWK 1029

RESULT 8
US-09-867-550-832
; Sequence 832, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehrahan, Ruad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells a
; FILE REFERENCE: 21402-013 (Cura-313)
```

;; CURRENT APPLICATION NUMBER: US/09/867,550
;; CURRENT FILING DATE: 2001-09-20
;; PRIOR APPLICATION NUMBER: USSN 60/208,427
;; PRIOR FILING DATE: 2000-05-30
;; NUMBER OF SEQ ID NOS: 2125
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 832
;; LENGTH: 137
;; TYPE: PRP
;; ORGANISM: Homo sapiens
US-09-867-550-832

Query Match 83.3%; Score 30; DB 10; Length 137;
Best Local Similarity 80.0%; Pred. No. 75;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWI 5
: 1111
DB 130 VFFWI 134

RESULT 9
US-09-393-634-51
;; Sequence 51, Application US/09393634
;; Patent No. US20020051997A1
;; GENERAL INFORMATION:
;; APPLICANT: Zuker, Charles S.
;; APPLICANT: Adler, Jon Elliot
;; APPLICANT: Ryba, Nick
;; APPLICANT: Mueller, Ken
;; APPLICANT: Hoon, Mark
;; APPLICANT: The Regents of the University of California
;; APPLICANT: as represented by the United States of America
;; APPLICANT: Department of Health and Human Services
;; TITLE OF INVENTION: SF, a No. US20020051997A1 Family of Taste Receptors
;; FILE REFERENCE: 02307E-09800005
;; CURRENT APPLICATION NUMBER: US/09/393,634
;; CURRENT FILING DATE: 1999-09-10
;; NUMBER OF SEQ ID NOS: 92
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 51
;; LENGTH: 312
;; TYPE: PRP
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: human GR09
US-09-393-634-51

Query Match 83.3%; Score 30; DB 10; Length 312;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFWIK 6
: 1111
DB 119 FFWIK 123

RESULT 10
US-09-992-598-177
;; Sequence 177, Application US/09992598
;; Patent No. US20020160384A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerltzen, Mary E.
;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC20
;; CURRENT APPLICATION NUMBER: US/09/992,598
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
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;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
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;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09

PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
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 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
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 PRIOR APPLICATION NUMBER: 60/090694
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 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090696
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090862
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 83.3%; Score 30; DB 9; Length 445;
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IFFWI 5
 Db 133 IFFWI 137

RESULT 11
 US-09-989-293A-177
 Sequence 177, Application US/09989293A
 Patent No. US20020177164A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Geiber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 83.3%; Score 30; DB 9; Length 145;
Best Local Similarity 80.0%; Pred. No. 2,1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFWT 5
||||:
DB 133 IFFWV 137

RESULT 12
US-10-063-547-32
Sequence 32, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
PRIOR FILING DATE: 2002-05-02
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 32
LENGTH: 445
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-547-32

Query Match 83.3%; Score 30; DB 9; Length 145;
Best Local Similarity 80.0%; Pred. No. 2,1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IFFWT 5
||||:
DB 133 IFFWV 137

RESULT 13
US-09-989-735-177
Sequence 177, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavrin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
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PRIOR APPLICATION NUMBER: 60/087609
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PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04

1 PRIOR APPLICATION NUMBER: 60/088026
2 PRIOR FILING DATE: 1998-06-04
3 PRIOR APPLICATION NUMBER: 60/088028
4 PRIOR FILING DATE: 1998-06-04
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7 PRIOR APPLICATION NUMBER: 60/088030
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9 PRIOR APPLICATION NUMBER: 60/088033
10 PRIOR FILING DATE: 1998-06-04
11 PRIOR APPLICATION NUMBER: 60/088326
12 PRIOR FILING DATE: 1998-06-04
13 PRIOR APPLICATION NUMBER: 60/088167
14 PRIOR FILING DATE: 1998-06-05
15 PRIOR APPLICATION NUMBER: 60/088202
16 PRIOR FILING DATE: 1998-06-05
17 PRIOR APPLICATION NUMBER: 60/088212
18 PRIOR FILING DATE: 1998-06-05
19 PRIOR APPLICATION NUMBER: 60/088217
20 PRIOR FILING DATE: 1998-06-05
21 PRIOR APPLICATION NUMBER: 60/088655
22 PRIOR FILING DATE: 1998-06-09
23 PRIOR APPLICATION NUMBER: 60/088734
24 PRIOR FILING DATE: 1998-06-10
25 PRIOR APPLICATION NUMBER: 60/088738
26 PRIOR FILING DATE: 1998-06-10
27 PRIOR APPLICATION NUMBER: 60/088742
28 PRIOR FILING DATE: 1998-06-10
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30 PRIOR FILING DATE: 1998-06-10
31 PRIOR APPLICATION NUMBER: 60/088824
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35 PRIOR APPLICATION NUMBER: 60/088858
36 PRIOR FILING DATE: 1998-06-11
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38 PRIOR FILING DATE: 1998-06-11
39 PRIOR APPLICATION NUMBER: 60/088876
40 PRIOR FILING DATE: 1998-06-11
41 PRIOR APPLICATION NUMBER: 60/089105
42 PRIOR FILING DATE: 1998-06-12
43 PRIOR APPLICATION NUMBER: 60/089440
44 PRIOR FILING DATE: 1998-06-16
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47 PRIOR APPLICATION NUMBER: 60/089514
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49 PRIOR APPLICATION NUMBER: 60/089532
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51 PRIOR APPLICATION NUMBER: 60/089538
52 PRIOR FILING DATE: 1998-06-17
53 PRIOR APPLICATION NUMBER: 60/089598
54 PRIOR FILING DATE: 1998-06-17
55 PRIOR APPLICATION NUMBER: 60/089599
56 PRIOR FILING DATE: 1998-06-17
57 PRIOR APPLICATION NUMBER: 60/089600
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59 PRIOR APPLICATION NUMBER: 60/089653
60 PRIOR FILING DATE: 1998-06-17
61 PRIOR APPLICATION NUMBER: 60/089801
62 PRIOR FILING DATE: 1998-06-18
63 PRIOR APPLICATION NUMBER: 60/089907
64 PRIOR FILING DATE: 1998-06-18
65 PRIOR APPLICATION NUMBER: 60/089908
66 PRIOR FILING DATE: 1998-06-18
67 PRIOR APPLICATION NUMBER: 60/089947
68 PRIOR FILING DATE: 1998-06-19
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70 PRIOR FILING DATE: 1998-06-19
71 PRIOR APPLICATION NUMBER: 60/089952
72 PRIOR FILING DATE: 1998-06-19
73 PRIOR APPLICATION NUMBER: 60/090246

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4 PRIOR APPLICATION NUMBER: 60/090254
5 PRIOR FILING DATE: 1998-06-22
6 PRIOR APPLICATION NUMBER: 60/090349
7 PRIOR FILING DATE: 1998-06-23
8 PRIOR APPLICATION NUMBER: 60/090355
9 PRIOR FILING DATE: 1998-06-23
10 PRIOR APPLICATION NUMBER: 60/090429
11 PRIOR FILING DATE: 1998-06-24
12 PRIOR APPLICATION NUMBER: 60/090431
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14 PRIOR APPLICATION NUMBER: 60/090435
15 PRIOR FILING DATE: 1998-06-24
16 PRIOR APPLICATION NUMBER: 60/090444
17 PRIOR FILING DATE: 1998-06-24
18 PRIOR APPLICATION NUMBER: 60/090445
19 PRIOR FILING DATE: 1998-06-24
20 PRIOR APPLICATION NUMBER: 60/090472
21 PRIOR FILING DATE: 1998-06-24
22 PRIOR APPLICATION NUMBER: 60/090535
23 PRIOR FILING DATE: 1998-06-24
24 PRIOR APPLICATION NUMBER: 60/090540
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27 PRIOR FILING DATE: 1998-06-24
28 PRIOR APPLICATION NUMBER: 60/090557
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56 PRIOR APPLICATION NUMBER: 60/091633
57 PRIOR FILING DATE: 1998-07-02
58 PRIOR APPLICATION NUMBER: 60/091978
59 PRIOR FILING DATE: 1998-07-07
60 PRIOR APPLICATION NUMBER: 60/091982
61 PRIOR FILING DATE: 1998-07-07
62 PRIOR APPLICATION NUMBER: 60/092182
63 PRIOR FILING DATE: 1998-07-09

Query Match 83.3%; Score 30; DB 9; Length 445;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IFFW 5
DB 133 IFFWV 137

RESULT 14
 US-09-990-444-177
 ; Sequence 177, Application US/09990444
 ; Publication No. US20020193300A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC19
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: US/09/990,444
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
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 ; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR APPLICATION NUMBER: 60/075945
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;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR APPLICATION NUMBER: 60/090472
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;;
Query Match 83.3%; Score 30; DB 9; Length 445;
Best Local Similarity 80.0%; Pred. No. 2,le+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 IFFWI 5
Db 133 IFFWI 137
RESULT 15
US-09-989-730-177
; Sequence 177, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
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Job time : 5.77273 secs

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